

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 06:59:55 ; Search time 2319 Seconds

(without alignments)
9319.114 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atggtaacggtcggtggc.....ttccaaacgtgaacatccg 446

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.prc.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 446 | 100.0 | 446 | 6 | BD223232 Method of |
| 2 | 446 | 100.0 | 446 | 6 | BD240919 Polynucle |
| 3 | 287.2 | 64.4 | 606 | 6 | BD223236 Method of |
| 4 | 284 | 63.7 | 557 | 6 | BD223246 Method of |
| 5 | 215.2 | 48.3 | 534 | 6 | BD223234 Method of |
| 6 | 215.2 | 48.3 | 534 | 6 | BD240936 Polynucle |
| 7 | 212 | 47.5 | 485 | 6 | BD223245 Method of |
| 8 | 177.2 | 39.7 | 577 | 6 | BD240918 Polynucle |
| 9 | 173.2 | 38.8 | 485 | 6 | BD223243 Method of |
| 10 | 172.2 | 38.6 | 446 | 6 | BD223239 Method of |
| 11 | 170 | 38.1 | 1093 | 6 | BD223244 Method of |
| 12 | 169.2 | 37.9 | 522 | 6 | BD223233 Method of |
| 13 | 168.6 | 37.8 | 460 | 6 | AX046745 Sequence |
| 14 | 168.6 | 37.8 | 503 | 6 | AX046743 Sequence |
| 15 | 167.2 | 37.5 | 534 | 6 | BD223237 Method of |
| 16 | 166 | 37.2 | 434 | 6 | BD223242 Method of |
| 17 | 166 | 37.2 | 437 | 6 | BD223241 Method of |
| 18 | 166 | 37.2 | 443 | 6 | BD223240 Method of |
| 19 | 166 | 37.2 | 488 | 6 | BD223248 Method of |

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|----|-------|------|-----|---|----------|-------------|
| 20 | 166 | 37.2 | 575 | 6 | BD223249 | Method of |
| 21 | 165.6 | 37.1 | 316 | 6 | BD223238 | Method of |
| 22 | 165.6 | 37.1 | 316 | 6 | BD240937 | Polynucle |
| 23 | 164 | 36.8 | 485 | 6 | BD223247 | Method of |
| 24 | 157.8 | 35.4 | 523 | 6 | BD240916 | Polynucle |
| 25 | 156.4 | 35.1 | 457 | 6 | AX046755 | Sequence |
| 26 | 156.4 | 35.1 | 463 | 6 | AX046751 | Sequence |
| 27 | 156.4 | 35.1 | 603 | 6 | AX046753 | Sequence |
| 28 | 154.8 | 34.7 | 458 | 6 | AX046763 | Sequence |
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| 33 | 153.2 | 34.3 | 464 | 6 | AX046761 | Sequence |
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| 36 | 138.4 | 31.0 | 439 | 6 | AX046757 | Sequence |
| 37 | 134.4 | 30.1 | 385 | 6 | BD240917 | Polynucle |
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| 40 | 99.4 | 22.3 | 150 | 6 | A39543 | Sequence 31 |
| 41 | 99.4 | 22.3 | 150 | 6 | AR050143 | Sequence |
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| 43 | 99.4 | 22.3 | 150 | 6 | BD240920 | Polynucle |
| 44 | 99.4 | 22.3 | 150 | 6 | I23718 | Sequence 31 |
| 45 | 91.4 | 20.5 | 150 | 6 | A26906 | C.benedictu |

ALIGNMENTS

| | | | | | | |
|------------|---|---|--------|-----|--------|-----------------|
| RESULT 1 | BD223232 | Method of genetic expression of polypeptide in plant. | 446 bp | DNA | linear | PAT 17-JUL-2003 |
| LOCUS | BD223232 | Method of genetic expression of polypeptide in plant. | | | | |
| DEFINITION | BD223232 | Method of genetic expression of polypeptide in plant. | | | | |
| ACCESSION | BD223232 | Method of genetic expression of polypeptide in plant. | | | | |
| VERSION | BD223232.1 | GI:33033002 | | | | |
| KEYWORDS | JP 2002523047-A/1. | | | | | |
| SOURCE | Dahlia merckii (bedding dahlia) | | | | | |
| ORGANISM | Dahlia merckii | | | | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsidae; Dahlia. | | | | | |
| AUTHORS | Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A. | | | | | |
| TITLE | Method of genetic expression of polypeptide in plant | | | | | |
| JOURNAL | Patent: JP 2002523047-A 1 30-JUL-2002; SYNGENTA LTD | | | | | |
| COMMENT | OS Dahlia merckii | | | | | |
| | PN JP 2002523047-A/1 | | | | | |
| | PD 30-JUL-2002 | | | | | |
| | PF 17-AUG-1999 JP 2000566429 | | | | | |
| | PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI | | | | | |
| | WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE | | | | | |
| | AUGUSTINE FRANCOIS, | | | | | |
| | PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI | | | | | |
| | ANTHONY RAY | | | | | |
| | PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC | | | | | |
| | C12R1:911, | | | | | |
| | PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91) | | | | | |
| | CC Method of genetic expression of polypeptide in plant FH Key | | | | | |
| | Location/Qualifiers | | | | | |
| FT CDS | (1)..(64) | | | | | |
| FT CDS | (157)..(446). | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
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Query Match 100.0%; Score 446; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTTCGCGGTTCTCGATCCCTTTTCGTCGCCATC 60
DB 1 ATGGTGAATCGGTGGTTCCTTCGCGGTTCTCGATCCCTTTTCGTCGCCATC 60

QY 61 TCAGGTTATCAAACTCTTAGTTCATTTATGAATAGATAGTATTTATTTATGG 120
DB 61 TCAGGTTATCAAACTCTTAGTTCATTTATGAATAGATAGTATTTATTTATGG 120

QY 121 TTTTATGTTCTGACAAAGTTGCAAAATATGAGTAGATATCGCATCCGTTAGTGGAAAC 180
DB 121 TTTTATGTTCTGACAAAGTTGCAAAATATGAGTAGATATCGCATCCGTTAGTGGAAAC 180

QY 181 TATCGGAGAAAGCTAGCAAGACATGTTCCGGAACCTGTGGCAATACGGGACATTTGTGACA 240
DB 181 TATCGGAGAAAGCTAGCAAGACATGTTCCGGAACCTGTGGCAATACGGGACATTTGTGACA 240

QY 241 ACCAATGTAATCATGGAGGGTGGGCCCATGAGCGGTGTCATGTGGTAAACGGGAAAC 300
DB 241 ACCAATGTAATCATGGAGGGTGGGCCCATGAGCGGTGTCATGTGGTAAACGGGAAAC 300

QY 301 ACATGTGTTCTGTACTTCAATTTGTAATAAGCGGAAAGCTTGTCTCAAGACAAACTTA 360
DB 301 ACATGTGTTCTGTACTTCAATTTGTAATAAGCGGAAAGCTTGTCTCAAGACAAACTTA 360

QY 361 AAGCGGAAACTCGCTCAAGACAACTTAATGCCCCAAAGCTTGACCGTATGCCAAGA 420
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QY 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446
DB 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446

RESULT 2
BD240919

LOCUS BD240919 446 bp DNA linear PAT 17-JUL-2003
DEFINITION Polynucleotide sequences.

ACCESSION BD240919

VERSION BD240919.1 GI:33050689

KEYWORDS Dalia merckii (bedding dahlia)

SOURCE Dalia merckii

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Coreopsidae; Dahlia.

1 (bases 1 to 446)

Evans, I.J. and Ray, J.A.

Polynucleotide sequences

Patent: JP 2002523052-A 5 30-JUL-2002;

SYNGENTA LTD

OS Dahlia merckii (dahlia)

PN JP 2002523052-A/5

PD 30-JUL-2002

PF 17-AUG-1999 JP 2000566448

PR 18-AUG-1998 GB 9818003.7

PI IAN JEFFREY EVANS, JOHN ANTHONY RAY

PC C12N15/09, A01H5/00, C07K14/415, C12N5/10/(C12N5/10, C12R1:91),

PC C12N15/00,

PC C12N5/00, (C12N5/00, C12R1:91)

CC Polynucleotide sequences

FH Key Location/Qualifiers

FT CDS (1)..(64)

FT CDS (157)..(446).

FEATURES

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1..446

/organism="Dahlia merckii"

/mol_type="genomic DNA"

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ORIGIN

Query Match 100.0%; Score 446; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTTCGCGGTTCTCGATCCCTTTTCGTCGCCATC 60
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QY 61 TCAGGTTATCAAACTCTTAGTTCATTTATGAATAGATAGTATTTATTTATGG 120
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DB 181 TATCGGAGAAAGCTAGCAAGACATGTTCCGGAACCTGTGGCAATACGGGACATTTGTGACA 240

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DB 241 ACCAATGTAATCATGGAGGGTGGGCCCATGAGCGGTGTCATGTGGTAAACGGGAAAC 300

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DB 301 ACATGTGTTCTGTACTTCAATTTGTAATAAGCGGAAAGCTTGTCTCAAGACAAACTTA 360

QY 361 AAGCGGAAACTCGCTCAAGACAACTTAATGCCCCAAAGCTTGACCGTATGCCAAGA 420
DB 361 AAGCGGAAACTCGCTCAAGACAACTTAATGCCCCAAAGCTTGACCGTATGCCAAGA 420

QY 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446
DB 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446

RESULT 3
BD223236

LOCUS BD223236 606 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.

ACCESSION BD223236

VERSION BD223236.1 GI:33033006

KEYWORDS JP 2002523047-A/5.

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 606)

Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and

Ray, J.A.

Method of genetic expression of polyprotein in plant

Patent: JP 2002523047-A 5 30-JUL-2002;

SYNGENTA LTD

OS Artificial Sequence

PN JP 2002523047-A/5

PD 30-JUL-2002

PF 17-AUG-1999 JP 2000566429

PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI

PI WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE

AUGUSTINE FRANCOIS,

PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI

ANTHONY RAY

PC C12N15/09, A01H1/00, C07K12, C12N5/10, C12P21/02/(C12N5/10, PC

C12R1:91),

PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)

CC Description of Artificial Sequence: Synthetic sequence FH

Key Location/Qualifiers

FT CDS (76)..(597).

FEATURES

source

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Best Local Similarity 99.0%; Pred. No. 1.1e-63;
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAGACATGGTGGGAAA 214
Db 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAGACATGGTGGGAAA 197

QY 215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 274
Db 198 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 257

QY 275 ACGGTGTTCATGTCGCTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 334
Db 258 ACGGTGTTCATGTCGCTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 317

QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 394
Db 318 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 377

QY 395 CCAAAAGCTTGACCGTGTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 446
Db 378 CCAAAAGCTTGACCGTGTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 429

RESULT 4
BD223246
LOCUS      557 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION  BD223246
VERSION     BD223246.1 GI:33033016
KEYWORDS   JP 2002523047-A/15.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 557)
AUTHORS    Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.
TITLE      Method of genetic expression of polyprotein in plant
JOURNAL    SYNGENTA LTD
COMMENT    OS Artificial Sequence
           PN JP 2002523047-A/15
           PD 30-JUL-2002
           PF 17-AUG-1999 JP 2000566429
           PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
           WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
           AUGUSTINE FRANCOIS,
           PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
           ANTHONY RAY
           PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC
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FEATURES
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Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 274
Db 198 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 257

QY 275 ACGGTGTTCATGTCGCTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 334
Db 258 ACGGTGTTCATGTCGCTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 317

QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 394
Db 318 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 377

QY 395 CCAAAAGCTTGACCGTGTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 446
Db 378 CCAAAAGCTTGACCGTGTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 429

RESULT 5
BD223234
LOCUS      534 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION  BD223234
VERSION     BD223234.1 GI:33033004
KEYWORDS   JP 2002523047-A/3.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 534)
AUTHORS    Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.
TITLE      Method of genetic expression of polyprotein in plant
JOURNAL    SYNGENTA LTD
COMMENT    OS Artificial Sequence
           PN JP 2002523047-A/3
           PD 30-JUL-2002
           PF 17-AUG-1999 JP 2000566429
           PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
           WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
           AUGUSTINE FRANCOIS,
           PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
           ANTHONY RAY
           PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC
           C12R1:91),
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FEATURES
source

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Best Local Similarity 98.6%; Pred. No. 5.2e-45;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAGACATGGTGGGAAA 197

QY 215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 274
Db 198 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAATCGCTCAAGACAACTTAATGC 257

QY 275 ACGGTGTTCATGTCGCTGATGCGGAAACACATGTTCTCTTACTTCAATTTGTAATAAGC 334
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QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 318 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 357

RESULT 6
LOCUS BD240936
DEFINITION Polynucleotide sequences.
ACCESSION BD240936
VERSION BD240936.1 GI:33050706
KEYWORDS JP 2002523052-A/22.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 534)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL
COMMENT SYNGENTA LTD
OS Artificial Sequence
PN JP 2002523052-A/22
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
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Best Local Similarity 98.6%; Pred. No. 5.2e-45;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 274
Db 198 CTGTGGCAACACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 257

QY 275 AGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTTTCAATTGTAATAAAGC 334
Db 258 AGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTTTCAATTGTAATAAAGC 317

QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 318 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 357

RESULT 7
LOCUS BD223245
DEFINITION Method of genetic expression of polypeptide in plant.
ACCESSION BD223245
VERSION BD223245.1 GI:33033015
KEYWORDS JP 2002523047-A/14.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 485)
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 318 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 357

RESULT 8
LOCUS BD240918
DEFINITION Polynucleotide sequences.
ACCESSION BD240918
VERSION BD240918.1 GI:33050688
KEYWORDS JP 2002523052-A/4.
SOURCE Dahlia merckii (bedding dahlia)
ORGANISM Dahlia merckii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiodeae; Dahlia.
REFERENCE 1 (bases 1 to 577)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002; SYNGENTA LTD
COMMENT OS Dahlia merckii (dahlia)
PN JP 2002523052-A/4
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, (C12N5/10, C12R1:91),
PC C12N5/00, (C12N5/00, C12R1:91)
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Key CDS Location/Qualifiers
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ORIGIN
Query Match 47.5%; Score 212; DB 6; Length 485;
Best Local Similarity 97.7%; Pred. No. 3.5e-44;
Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
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QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 274
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QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 245 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 284

RESULT 9
LOCUS BD240918
DEFINITION Polynucleotide sequences.
ACCESSION BD240918
VERSION BD240918.1 GI:33050688
KEYWORDS JP 2002523052-A/4.
SOURCE Dahlia merckii (bedding dahlia)
ORGANISM Dahlia merckii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiodeae; Dahlia.
REFERENCE 1 (bases 1 to 577)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002; SYNGENTA LTD
COMMENT OS Dahlia merckii (dahlia)
PN JP 2002523052-A/4
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, (C12N5/10, C12R1:91),
PC C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key CDS Location/Qualifiers
FT CDS Location/Qualifiers
1. .485
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/mol_type="genomic DNA"
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Best Local Similarity 97.7%; Pred. No. 3.5e-44;
Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCTCACGG 184

QY 275 AGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTTTCAATTGTAATAAAGC 334
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QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 245 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 284

RESULT 10
LOCUS BD240918
DEFINITION Polynucleotide sequences.
ACCESSION BD240918
VERSION BD240918.1 GI:33050688
KEYWORDS JP 2002523052-A/4.
SOURCE Dahlia merckii (bedding dahlia)
ORGANISM Dahlia merckii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiodeae; Dahlia.
REFERENCE 1 (bases 1 to 577)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002; SYNGENTA LTD
COMMENT OS Dahlia merckii (dahlia)
PN JP 2002523052-A/4
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, (C12N5/10, C12R1:91),
PC C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key CDS Location/Qualifiers
FT CDS Location/Qualifiers
1. .485
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 47.5%; Score 212; DB 6; Length 485;
Best Local Similarity 97.7%; Pred. No. 3.5e-44;
Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCTCACGG 184

QY 275 AGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTTTCAATTGTAATAAAGC 334
Db 185 AGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTTTCAATTGTAATAAAGC 244

QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 374
Db 245 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGACCAACTC 284
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FH Key Location/Qualifiers
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Best Local Similarity 80.1%; Pred. No. 3.7e-35;
Matches 234; Conservative 0; Mismatches 28; Indels 30; Gaps 1;
QY 155 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 82 AGATATCAACAGTGTGAGAGGAGAGTATGCGAGAAAGCTAGCAAGACATGTCAGGAAA 141
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCTATGCGAGGGTGGCGCCCATGG 274
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QY 275 AGCGTGTCTATGTCGTAACCGGAAACACATGTTTCTGTTACTTCAATTTGTAAGAAAGC 334
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QY 335 CGAAAGACTTGTCTCAAGCAAACTTAAGCCGACAACTCGCTCAAGACAAACTTAATGC 394
Db 262 CGAAAGACTT-----GCTCAAGACAAAGTGAATGC 291
QY 395 CCAAGAGCTTGACCGTGTGATGCCAAGAAAGTATTCGAACGTTGAACATCCG 446
Db 292 CCAAGAGCTTGACCGTGTGATGCCAAGAAAGTATTCGAACGTTGAACATCCG 343
RESULT 9
BD223243
LOCUS 485 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223243
VERSION BD223243.1 GI:33033013
KEYWORDS JP 2002523047-A/12.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 485)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/12
PD 30-JUL-2002
PP 17-AUG-1999 JP 2000566429 9826753.7 PI
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key Location/Qualifiers
FT CDS (3)..(476).
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Best Local Similarity 93.3%; Pred. No. 7.3e-34;
Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Db 65 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124
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Best Local Similarity 85.1%; Pred. No. 4e-34; Mismatches 33; Indels 3; Gaps 1;
Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;
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Db 65 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCTATGCGAGGGTGGCGCCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGTGACCAACCAATGTAATCTATGCGAGGGTGGCGCCCATGG 184
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Db 195 AGCGTGTCTATGTCGTAACCGGAAACACATGTTTCTGTTACTTCAATTTGTTGTAACGC 244
QY 335 CGAAAGACTTGTCTCAAGCAAACTTTAAAG---CCGAAACAACTCGCTCAAGACAAACTTTAA 391
Db 245 TGAGGAAGCTGCTGCTGCTATTCTCTGAAGCTTCTGAAGAACTTGTCTCAAGAAAGACTCC 304
QY 392 TG 393
Db 305 TG 306
RESULT 10
BD223239
LOCUS 446 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223239
VERSION BD223239.1 GI:33033009
KEYWORDS JP 2002523047-A/8.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 446)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/8
PD 30-JUL-2002
PP 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key Location/Qualifiers
FT CDS (3)..(437).
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Query Match 38.6%; Score 172.2; DB 6; Length 446;
Best Local Similarity 93.3%; Pred. No. 7.3e-34;
Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 155 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
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QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCTATGCGAGGGTGGCGCCCATGG 274
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Db 125 CTGTGGCAACAGCGGACATTGTGACAAACAATGTAATCATGGAGGGTGGCGCTCAGG 184
 QY 275 AGCGTGTCTATGCGCTAAGCGGAAACACACATGTTTCTGTTACTTCAATTGTAATAAAGC 334
 Db 185 AGCGTGTCTATGCGCTAAGCGGAAACACACATGTTTCTGTTACTTCAATTGTAAGCGGC 244
 QY 335 CGAAAAGCTTGGT 347
 Db 245 CGACGAGTGGCT 257

RESULT 11
 LOCUS BD223244
 DEFINITION Method of genetic expression of polypeptide in plant.
 ACCESSION BD223244
 VERSION BD223244.1 GI:33033014
 KEYWORDS JP 2002523047-A/13.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 1093)
 AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.
 TITLE Method of genetic expression of polypeptide in plant
 JOURNAL SINGENTA LTD
 COMMENT OS Artificial Sequence
 PN JP 2002523047-A/13
 PD 30-JUL-2002
 PF 17-AUG-1999 JP 2000566429
 PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
 WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
 AUGUSTINE FRANCOIS,
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
 ANTHONY RAY
 PC C12N15/00, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC
 C12R1:91),
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 Key Location/Qualifiers
 FT CDS (3)..(1085).

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 Best Local Similarity 84.3%; Pred. No. 2.8e-33;
 Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
 QY 155 AGATATCGCATCCGTTAGTGAGAACTATCGGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
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 QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCGCTCAGG 184
 Db 125 CTGTGGCAACAGCGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCGCTCAGG 184
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 Db 185 AGCGTGTCTATGCGCTAAGCGGAAACACATGTTTCTGTTACTTCAACTGCGCTAACGC 244
 QY 335 CGAAAAGCTTCAAGCAACTTAAG---CCGAACCACTCGCTCAAGCAAACTTAA 391
 Db 245 TGAGGAAGCTGCTGCTGCTATTCTTGAAGCTTCTGAAGAACTTGTCTCAAGAAAGCTCC 304
 QY 392 TG 393
 Db 305 TG 306

RESULT 12
 LOCUS BD223233
 DEFINITION Method of genetic expression of polypeptide in plant.
 ACCESSION BD223233
 VERSION BD223233.1 GI:33033003
 KEYWORDS JP 2002523047-A/2.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 522)
 AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.
 TITLE Method of genetic expression of polypeptide in plant
 JOURNAL SINGENTA LTD
 COMMENT OS Artificial Sequence
 PN JP 2002523047-A/2
 PD 30-JUL-2002
 PF 17-AUG-1999 JP 2000566429
 PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
 WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
 AUGUSTINE FRANCOIS,
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
 ANTHONY RAY
 PC C12N15/00, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC
 C12R1:91),
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 Key Location/Qualifiers
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 ORIGIN

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 Db 138 AGATATCGCATCCGTTAGTGAGAACTATCGGAGAAAGCTAGCAAGCATGGTCGGGAAA 197
 QY 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCGCTCAGG 274
 Db 198 CTGTGGCAACAGCGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCGCTCAGG 257
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 QY 335 CG 336
 Db 318 TG 319

RESULT 13
 LOCUS AX046745
 DEFINITION Sequence 3 from Patent WO0068405.
 ACCESSION AX046745
 VERSION AX046745.1 GI:11876281
 KEYWORDS Dimorphanthea sinuata (African daisy)
 SOURCE Dimorphanthea sinuata
 ORGANISM Dimorphanthea sinuata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteraceae;
 Calenduleae; Dimorphanthea.

Query Match 37.9%; Score 169.2; DB 6; Length 522;
 Best Local Similarity 95.6%; Pred. No. 4.4e-33;
 Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 155 AGATATCGCATCCGTTAGTGAGAACTATCGGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
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 Db 318 TG 319

RESULT 13
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 ACCESSION AX046745
 VERSION AX046745.1 GI:11876281
 KEYWORDS Dimorphanthea sinuata (African daisy)
 SOURCE Dimorphanthea sinuata
 ORGANISM Dimorphanthea sinuata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteraceae;
 Calenduleae; Dimorphanthea.

REFERENCE 1
AUTHORS Miao,G.H., Weng,Z. and Famodu,O.O.
TITLE Plant defensins
JOURNAL Patent: WO 0068405-A 3 16-NOV-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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Best Local Similarity 81.6%; Pred. No. 6.3e-33;
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QY 215 CTGTGGCAATACGGACATTTGTGACAAACCAATGTAATCATGGGAGGTCGGGCCCATGG 274
DB 147 CTGTGGCAACACGGGACACTGTGAGCAGCAGTGAAGTCGTGGGAGACTGCAGGCCCATGG 206
QY 275 AGCGTGTCATGTCGTAAACGGGAAACACATGTTCTGTACTTCAATTGTAAGAAAGC 334
DB 207 TCGGTGTCATGTCGTGGTGGGAAACACATGTCGTACTTCAATTGTAAGAAAGC 266
QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGACAACTTAAATG 393
DB 267 CGAAAGCTTGTCCCAAGACAAGCTCAACGCTGAAAAATTCGGCCGTGATGAGTTAAAG 325
RESULT 14
AX046743
LOCUS AX046743 503 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 1 from Patent WO0068405.
ACCESSION AX046743
VERSION AX046743.1 GI:11876280
KEYWORDS
SOURCE Dimorphotheca sinuata (African daisy)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Dimorphotheca.
REFERENCE 1
AUTHORS Miao,G.H., Weng,Z. and Famodu,O.O.
TITLE Plant defensins
JOURNAL Patent: WO 0068405-A 1 16-NOV-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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Query Match 37.8%; Score 168.6; DB 6; Length 503;
Best Local Similarity 81.6%; Pred. No. 6.3e-33;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGAAA 214
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QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGCGGAGGTCGGGCCCATGG 274
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QY 275 AGCGTGTCATGTCGTAAACGGGAAACACATGTTCTGTACTTCAATTGTAAGAAAGC 334
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QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGACAACTTAAATG 393
DB 260 CGAAAGCTTGTCCCAAGACAAGCTCAACGCTGAAAAATTCGGCCGTGATGAGTTAAAG 318
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BD223237
LOCUS BD223237 534 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223237
VERSION BD223237.1 GI:33033007
KEYWORDS JP 2002523047-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 534)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL Patent: JP 2002523047-A 6 30-JUL-2002;
SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/6
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02//C12N5/10, PC
C12R1:91)
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key Location/Qualifiers
FT CDS (76)..(525).
FEATURES
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Matches 169; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004as:.*
13: geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 446 | 100.0 | 446 | AAZ51379 | Dahlia me |
| 2 | 446 | 100.0 | 446 | AAZ99332 | AAZ99332 DNA encod |
| 3 | 287.2 | 64.4 | 606 | AAZ99326 | AAZ99326 DNA encod |
| 4 | 284 | 63.7 | 557 | AAZ99336 | AAZ99336 DNA encod |
| 5 | 215.2 | 48.3 | 534 | AAZ51396 | AAZ51396 Portion o |
| 6 | 215.2 | 48.3 | 534 | AAZ99325 | AAZ99325 DNA encod |
| 7 | 212 | 47.5 | 485 | AAZ99335 | AAZ99335 DNA encod |
| 8 | 209.4 | 47.0 | 529 | Adm77231 | Adm77231 Ironweed |
| 9 | 203 | 45.5 | 579 | Adm77214 | Adm77214 Ironweed |
| 10 | 177.2 | 39.7 | 577 | AAZ51378 | AAZ51378 Dahlia me |
| 11 | 173.2 | 38.8 | 485 | AAZ99333 | AAZ99333 DNA encod |
| 12 | 172.2 | 38.6 | 446 | AAZ99329 | AAZ99329 DNA encod |
| 13 | 170 | 38.1 | 1093 | AAZ99334 | AAZ99334 DNA encod |
| 14 | 169.2 | 37.9 | 522 | AAZ99324 | AAZ99324 DNA encod |
| 15 | 168.6 | 37.8 | 460 | AAZ54387 | AAZ54387 Plant def |
| 16 | 168.6 | 37.8 | 460 | Adm77186 | Adm77186 African d |
| 17 | 168.6 | 37.8 | 503 | AAZ54386 | AAZ54386 Plant def |
| 18 | 168.6 | 37.8 | 503 | Adm77184 | Adm77184 African d |
| 19 | 167.2 | 37.5 | 534 | AAZ99327 | AAZ99327 DNA encod |
| 20 | 166 | 37.2 | 434 | AAZ99332 | AAZ99332 DNA encod |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 21 | 166 | 37.2 | 437 | 3 | AAZ99331 | AAZ99331 DNA encod |
| 22 | 166 | 37.2 | 443 | 3 | AAZ99330 | AAZ99330 DNA encod |
| 23 | 166 | 37.2 | 488 | 3 | AAZ99338 | AAZ99338 DNA encod |
| 24 | 166 | 37.2 | 575 | 3 | AAZ99339 | AAZ99339 DNA encod |
| 25 | 165.6 | 37.1 | 316 | 3 | AAZ51397 | AAZ51397 Portion o |
| 26 | 165.6 | 37.1 | 316 | 3 | AAZ99328 | AAZ99328 DNA of pF |
| 27 | 164 | 36.8 | 485 | 3 | AAZ99337 | AAZ99337 DNA encod |
| 28 | 161 | 36.1 | 461 | 11 | Adm77229 | Adm77229 Sunflower |
| 29 | 157.8 | 35.4 | 523 | 3 | AAZ51376 | AAZ51376 Dahlia me |
| 30 | 156.4 | 35.1 | 457 | 5 | AAZ54392 | AAZ54392 Plant def |
| 31 | 156.4 | 35.1 | 457 | 11 | Adm77196 | Adm77196 Mexican r |
| 32 | 156.4 | 35.1 | 463 | 5 | AAZ54390 | AAZ54390 Plant def |
| 33 | 156.4 | 35.1 | 463 | 11 | Adm77192 | Adm77192 Mexican r |
| 34 | 156.4 | 35.1 | 603 | 5 | AAZ54391 | AAZ54391 Plant def |
| 35 | 156.4 | 35.1 | 603 | 11 | Adm77194 | Adm77194 Mexican r |
| 36 | 154.8 | 34.7 | 458 | 5 | AAZ54396 | AAZ54396 Plant def |
| 37 | 154.8 | 34.7 | 458 | 11 | Adm77204 | Adm77204 Mexican r |
| 38 | 154.8 | 34.7 | 460 | 5 | AAZ54394 | AAZ54394 Plant def |
| 39 | 154.8 | 34.7 | 460 | 11 | Adm77200 | Adm77200 Mexican r |
| 40 | 154.2 | 34.6 | 565 | 5 | AAZ84841 | AAZ84841 Sunflower |
| 41 | 153.2 | 34.3 | 464 | 5 | AAZ54395 | AAZ54395 Plant def |
| 42 | 153.2 | 34.3 | 464 | 11 | Adm77202 | Adm77202 Mexican r |
| 43 | 153.2 | 34.3 | 472 | 5 | AAZ54397 | AAZ54397 Plant def |
| 44 | 153.2 | 34.3 | 472 | 11 | Adm77206 | Adm77206 Mexican r |
| 45 | 146.8 | 32.9 | 399 | 3 | AAZ51375 | AAZ51375 Dahlia me |

ALIGNMENTS

RESULT 1
AAZ51379
ID AAZ51379 standard; DNA; 446 BP.
XX
AC AAZ51379;
XX
DT 06-JUN-2000 (first entry)
XX
DE Dahlia merckii antimicrobial protein Dm-AMPI gene.
XX
KW Antimicrobial protein; Dm-AMPI; transgenic plant; microbial infection;
KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
KW apple; ds.
XX
OS Dahlia merckii.
XX
FH Key
FT CDS
FT
FT Location/Qualifiers
FT 1..446
FT /*tag= a
FT /product= "Antimicrobial protein Dm-AMPI"
FT /note= "Does not include stop codon"
FT /partial
FT sig_peptide 1..176
FT FT /*tag= e
FT /note= "excludes intron"
FT exon 1..64
FT /*tag= b
FT /number= 1
FT intron 65..156
FT /*tag= c
FT /number= 1
FT exon 157..446
FT /*tag= d
FT /number= 2
FT mat_peptide 177..326
FT /*tag= f
FT /product= "Mature Dm-AMPI protein"
FT misc_feature 327..446
FT /*tag= g
FT /note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"
XX
PN WO200011196-A1.

```
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002720.
XX PR 18-AUG-1999; 98GB-00018003.
XX (ZENE ) ZENECA LTD.
XX PA Evans IJ, Ray JA;
XX PI
XX FT WPI; 2000-237658/20.
XX DR P-PSDB; AAY70315.
XX PT Polynucleotide sequences and expression products useful for producing
XX transgenic plants that are resistant to microbial infections.
XX PS Claim 1; Fig 1A; 77pp; English.
XX CC The present sequence is a Dahlia merckii cDNA encoding an antimicrobial
XX preprotein Dm-AMPI. This sequence is useful in the production of
XX transgenic plants which show improved resistance to infections by
XX microorganisms such as bacteria and fungi. Transgenic plants include e.g.
XX field crops, fruits and vegetables, such as canola, sunflower, tomato,
XX apple, banana, pear and mango
XX SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;

Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCCTGATCCCTTTTCGTCTGCCCATC 60
DB 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCCTGATCCCTTTTCGTCTGCCCATC 60

QY 61 TCAGGTTATCAATCTTTAGTTCAATTTATGAATATGATAGTATTTATTTATTTATGG 120
DB 61 TCAGGTTATCAATCTTTAGTTCAATTTATGAATATGATAGTATTTATTTATTTATGG 120

QY 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCCTTTAGTGAGAAC 180
DB 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCCTTTAGTGAGAAC 180

QY 181 TATGCGAAGACTAGCAAGACATGTCGGAACCTGCGCAATACGGACATTTGTGACA 240
DB 181 TATGCGAAGACTAGCAAGACATGTCGGAACCTGCGCAATACGGACATTTGTGACA 240

QY 241 ACCAATGTAATCATGGAGGGTGGCGCCCATGGAGCGTGTGATGTAACGGGAAC 300
DB 241 ACCAATGTAATCATGGAGGGTGGCGCCCATGGAGCGTGTGATGTAACGGGAAC 300

QY 301 ACATGTGTTCTGTTACTTCAATTTGTAATAAAGCGGAAAGCTTCTCAAGACAACTTA 360
DB 301 ACATGTGTTCTGTTACTTCAATTTGTAATAAAGCGGAAAGCTTCTCAAGACAACTTA 360

QY 361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCCCAAAAGCTTCAACCGTATGCCAGA 420
DB 361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCCCAAAAGCTTCAACCGTATGCCAGA 420

QY 421 AAGTGGTTCCAAACGTTGAACATCCG 446
DB 421 AAGTGGTTCCAAACGTTGAACATCCG 446
```

RESULT 2

```
AAZ99323
ID AAZ99323 standard; DNA; 446 BP.
XX AC AAZ99323;
XX DT 03-JUL-2000 (first entry)
XX
```

DNA encoding the Dahlia antimicrobial protein 1 (AMPI).

Antimicrobial protein; AMPI; transgenic plant; linker propeptide; protein expression; ss.

Dahlia merckii.

Key Location/Qualifiers
CDS 1..446
/tag= a
/note= "contains 1 intron; no termination codon"
exon 1..64
/tag= b
intron 65..156
/tag= c
exon 157..446
/tag= d
mat_peptide 177..314
/tag= e

WO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99WO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENE) ZENECA LTD.

Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
WPI; 2000-246564/21.
P-PSDB; AAY84050.

Improving expression of polypeptides in plants involves coexpression of two or more proteins in plants within a single transcription unit.

Example 1; Fig 1; 151pp; English.

The present sequence encodes a Dahlia antimicrobial protein (AMP) 1. The AMP1 protein is used to produce transgenic plants, using the method of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence

Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;

Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCCTGATCCCTTTTCGTCTGCCCATC 60
DB 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCCTGATCCCTTTTCGTCTGCCCATC 60
QY 61 TCAGGTTATCAATCTTTAGTTCAATTTATGAATATGATAGTATTTATTTATTTATGG 120
DB 61 TCAGGTTATCAATCTTTAGTTCAATTTATGAATATGATAGTATTTATTTATTTATGG 120
QY 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCCTTTAGTGAGAAC 180

Db 121 TTTTATGTTCTGACAGATGTCACAAATATTGAGTAGATATCCATCCGTTAGTGAGAAC 180
 Qy 181 TATCGAGAAAGCTAGCAAGACATGTCGGGAAATGTCGGCAATACGGGACATTTGTGACA 240
 Db 181 TATCGAGAAAGCTAGCAAGACATGTCGGGAAATGTCGGCAATACGGGACATTTGTGACA 240
 Qy 241 ACCAATGTAATCATGGGAGGTCGGCCCATGGAGCGTGTCTATGTCGTAACGGGAAAC 300
 Db 241 ACCAATGTAATCATGGGAGGTCGGCCCATGGAGCGTGTCTATGTCGTAACGGGAAAC 300
 Qy 301 ACATGTTGTTCTGTTACTTCAATTTGTAATAAGCCGAAAGCTTGTCTCAAGACAACTTA 360
 Db 301 ACATGTTGTTCTGTTACTTCAATTTGTAATAAGCCGAAAGCTTGTCTCAAGACAACTTA 360
 Qy 361 AAGCCGAAACATCGCTCAAGACAACTTAATGTCGCAAAAGCTTCAACCGTGTGCAAGA 420
 Db 361 AAGCCGAAACATCGCTCAAGACAACTTAATGTCGCAAAAGCTTCAACCGTGTGCAAGA 420
 Qy 421 AAGTGGTTCCTCAACCTTGAACATCCG 446
 Db 421 AAGTGGTTCCTCAACCTTGAACATCCG 446

RESULT 3

ID AAZ993326 standard; DNA; 606 BP.
 AC AAZ993326;

DT 03-JUL-2000 (first entry)
 XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

DE Antimicrobial protein; AMP1; transgenic plant; linker propeptide;

KW protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.
 XX Synthetic.

OS Dahlia merckii.
 OS Unidentified.

FH Key Location/Qualifiers
 FT CDS 76..597
 FT /*tag= a
 FT misc_feature 160..309
 FT /*tag= b
 FT /note= "encodes DmAMP1"
 FT misc_feature 442..594
 FT /*tag= c
 FT /note= "encodes RsAPP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

XX 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84059.

XX Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

XX Example 2; Fig 11; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the

CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence

XX Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;

Query Match 64.4%; Score 287.2; DB 3; Length 606;
 Best Local Similarity 99.0%; Pred. No. 6.1e-69;

Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 155 AGATATCGATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214

Db 138 AGATATCGATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 197

Qy 215 CTGTGGCAATACGGGACATTTGTCAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274

Db 198 CTGTGGCAACACGGGACATTTGTCAACCAATGTAATCATGGAGGGTGGCGCCCATGG 257

Qy 275 AGCGTGTCTATGTCGTAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAATAAAGC 334

Db 258 AGCGTGTCTATGTCGTAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAATAAAGC 317

Qy 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 394

Db 318 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 377

Qy 395 CCNAAAGCTTGACCGTGATGCCNAGAAAGTGGTCCNAAAGCTTGACATCCG 446

Db 378 CCNAAAGCTTGACCGTGATGCCNAGAAAGTGGTCCNAAAGCTTGACATCCG 429

RESULT 4

AAZ99336
 ID AAZ99336 standard; DNA; 557 BP.

AC AAZ99336;

XX 03-JUL-2000 (first entry)

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

DE Antimicrobial protein; AMP1; transgenic plant; linker propeptide;

KW protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

FH Key Location/Qualifiers

FT CDS 3..548

FT /*tag= a

FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

XX 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.


```
FT misc_feature 160..309
FT /*tag= b
FT /note= "encodes DmAMP1"
FT misc_feature 370..538
FT /*tag= c
FT /note= "encodes RsAPP2"
XX
XX WO200011175-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 17-AUG-1999; 99WO-GB002716.
XX
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84058.
XX
XX Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX
XX Example 2; Fig 9; 151pp; English.
XX
XX The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
XX
XX Query Match 48.3%; Score 215.2; DB 3; Length 534;
XX Best Local Similarity 98.6%; Pred. No. 4e-49;
XX Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
XX |||||||
XX DB 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 197
XX |||||||
XX
XX QY 215 CTGTGCGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
XX |||||||
XX DB 198 CTGTGCGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 257
XX |||||||
XX
XX QY 275 AGCGTGTCTATGTCGTAACCGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 334
XX |||||||
XX DB 258 AGCGTGTCTATGTCGTAACCGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 317
XX |||||||
XX
XX QY 335 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 374
XX |||||||
XX DB 318 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 357
XX |||||||
XX
XX RESULT 7
XX AAZ99335
XX ID AAZ99335 standard; DNA; 485 BP.
XX
XX AC AAZ99335;
XX
XX 03-JUL-2000 (first entry)
```

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;

XX protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.

XX Synthetic.

XX Dahlia merckii.

XX Unidentified.

XX Key Location/Qualifiers

XX CDS 3..476

XX /*tag= a

XX /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX

XX PD 02-MAR-2000.

XX

XX PF 17-AUG-1999; 99WO-GB002716.

XX

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX

XX PA (ZENE) ZENECA LTD.

XX

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84068.

XX

XX Improving expression of polyproteins in plants involves coexpression of

XX two or more proteins in plants within a single transcription unit.

XX

XX Disclosure; Fig 30; 151pp; English.

XX

XX The present sequence encodes a protein of the invention, comprising the

XX mature proteins of the plant defensins, the Dahlia antimicrobial protein

XX (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker

XX propeptide of the invention. The specification describes methods for

XX improving expression levels of one or more proteins in a transgenic

XX plant. The method comprises inserting a DNA sequence having a promoter

XX region operably linked to two or more protein encoding regions separated

XX by a DNA sequence coding for a linker propeptide and a terminator region.

XX The method is used to produce proteins in plants. The linker propeptide

XX comprising a cleavage site, whereby the expressed polypeptide is post-

XX translationally processed into the component protein molecules. The

XX propeptide sequence is rich in amino acids A, V, S and T and contains

XX dipeptidic sequences consisting of either two acidic, two basic or one

XX acidic and one basic residue as a cleavable linker sequence

XX

XX Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;

XX

XX Query Match 47.5%; Score 212; DB 3; Length 485;

XX Best Local Similarity 97.7%; Pred. No. 3e-48;

XX Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX

XX QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214

XX |||||||

XX DB 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124

XX |||||||

XX

XX QY 215 CTGTGCGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274

XX |||||||

XX DB 125 CTGTGCGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGGCTCACGG 184

XX |||||||

XX

XX QY 275 AGCGTGTCTATGTCGTAACCGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 334

XX |||||||

XX DB 185 AGCGTGTCTATGTCGTAACCGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 244

XX |||||||

XX

XX QY 335 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 374

XX |||||||

XX DB 245 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 284

XX |||||||

```
RESULT 8
ADM77231
ID ADM77231 standard; cDNA; 529 BP.
XX
XX
AC ADM77231;
XX
XX 03-JUN-2004 (first entry)
XX
XX Ironweed cDNA encoding mature defensin #2.
XX
XX Ironweed; ss; EST; expressed sequence tag; defensin;
XX soybean cyst nematode; pesticide; plant; plant pathogen;
XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.
XX
XX Vernonia mespilifolia.
XX
XX US2003140368-A1.
XX
XX 24-JUL-2003.
XX
XX 21-JUN-2002; 2002US-00178449.
XX
XX 25-OCT-2001; 2001US-00030516.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Famodu OO, Herrmann R, Lu AL, Mccutchen BF, Miao G, Presnail JK;
XX PI Rafaleki JA, Weng Z;
XX
XX WPI; 2003-851760/79.
XX P-PSDB; ADM77232.
XX
XX New nucleic acid molecule, useful for preparing a composition for
XX treating fungal infections, e.g. Candidiasis.
XX
XX Claim 1; SEQ ID NO 48; 69pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (either an
XX EST, expressed sequence tag or an EST contig) encoding a plant defensin
XX or its mature form, or the complement of them. Also included are a DNA
XX construct comprising the novel nucleic acid (operably linked to a
XX promoter that drives expression in a host cell), an expression cassette
XX comprising the DNA construct, a host cell having stably incorporated into
XX its genome the DNA construct, an isolated polypeptide and impacting a
XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The
XX nucleic acid construct is useful for preparing a composition for treating
XX fungal infections, e.g. Candidiasis. The present sequence is either an
XX EST (expressed sequence tag) or an EST contig encoding a plant defensin
XX or its mature form.
XX
XX Sequence 529 BP; 178 A; 88 C; 111 G; 148 T; 0 U; 4 Other;
XX
XX Query Match 47.0%; Score 209.4; DB 11; Length 529;
XX Best Local Similarity 82.5%; Pred. No. 1.6e-47;
XX Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
XX
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAA 214
DB 78 AGAAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAAAGCTAGCAAGACATGGTCAGGCAA 137
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
DB 138 CTGTGGCAACACAGGACATTTGTGATNATCAGTGTAACTCATGGAGGGTGGCGCCATGG 197
QY 275 AGCGTGTGATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
DB 198 AGCTTGTGATGTGCGTGGAGGAAACACATGTGCTTTTGTATTTCATTTGTAAGGAAAGC 257
QY 335 CGAAAAGCTTCTCAAGCAACACTTAAAGCCGACAACTCGCTCAAGACAACTTAATGCG 394
DB 258 TGAAAAAATCTCGTCAAGTAAAGCTAAAGGAGAGAGCTTGTCTAAAGCAAACTCAAGGC 317

RESULT 9
ADM77214
ID ADM77214 standard; cDNA; 579 BP.
XX
XX
AC ADM77214;
XX
XX 03-JUN-2004 (first entry)
XX
XX Ironweed cDNA encoding mature defensin #1.
XX
XX Ironweed; ss; EST; expressed sequence tag; defensin;
XX soybean cyst nematode; pesticide; plant; plant pathogen;
XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.
XX
XX Vernonia mespilifolia.
XX
XX US2003140368-A1.
XX
XX 24-JUL-2003.
XX
XX 21-JUN-2002; 2002US-00178449.
XX
XX 25-OCT-2001; 2001US-00030516.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Famodu OO, Herrmann R, Lu AL, Mccutchen BF, Miao G, Presnail JK;
XX PI Rafaleki JA, Weng Z;
XX
XX WPI; 2003-851760/79.
XX P-PSDB; ADM77215.
XX
XX New nucleic acid molecule, useful for preparing a composition for
XX treating fungal infections, e.g. Candidiasis.
XX
XX Claim 1; SEQ ID NO 31; 69pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (either an
XX EST, expressed sequence tag or an EST contig) encoding a plant defensin
XX or its mature form, or the complement of them. Also included are a DNA
XX construct comprising the novel nucleic acid (operably linked to a
XX promoter that drives expression in a host cell), an expression cassette
XX comprising the DNA construct, a host cell having stably incorporated into
XX its genome the DNA construct, an isolated polypeptide and impacting a
XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The
XX nucleic acid construct is useful for preparing a composition for treating
XX fungal infections, e.g. Candidiasis. The present sequence is either an
XX EST (expressed sequence tag) or an EST contig encoding a plant defensin
XX or its mature form.
XX
XX Sequence 579 BP; 198 A; 97 C; 117 G; 167 T; 0 U; 0 Other;
XX
XX Query Match 45.5%; Score 203; DB 11; Length 579;
XX Best Local Similarity 81.1%; Pred. No. 9.5e-46;
XX Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
XX
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCAGGCAA 214
DB 92 AGAAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAGAGCTAGCAAGACATGGTCAGGCAA 151
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
DB 152 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAACTCATGGAGGGTGGCGCCATGG 211
QY 275 AGCGTGTGATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
DB 212 AGCTTGTGATGTGCGTGGAGGAAACACATGTGCTTTTGTCTATTTCATTTGTAAAAAGC 271
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QY 335 CGAAGAGCTTGCTCAAGCAAACTTAAGCCGAAACACTCGCTCAAGCAAACTTAATGC 394
 DB 272 TGAAGAACTCGCTCAAGTAAGTTAAAGCTGAAGAGCTTGCAAAAGCAAACTCAAGGC 331
 QY 395 CCAAGAGCTTGACCGTGATGCCAAGAAAGTGTTCCAAACGTTGAACATCC 445
 DB 332 AGATAAGTTTGACCATGATGCAAGAGAGTAGTACCAATGTCGAACATCC 382

RESULT 10

AAZ51378
 ID AAZ51378 standard; cDNA; 577 BP.

XX AAZ51378;

DT 06-JUN-2000 (first entry)

XX Dahlia merckii antimicrobial protein Dm2.5 cDNA.

XX Antimicrobial protein; DmAMP; Dm2.5; transgenic plant;
 KW microbial infection; bacteria; fungi; field crop; fruit; vegetable;
 KW canola; banana; sunflower; apple; ss.
 XX Dahlia merckii.

XX Key Location/Qualifiers
 FH CDS 20..346

FT /*tag= a
 FT /product= "Antimicrobial protein Dm2.5"
 FT /note= "Preproprotein"

FT sig_peptide 20..103

FT mat_peptide 104..253
 FT /*tag= c

FT misc_feature 254..343
 FT /product= "Mature Dm2.5 protein"

FT /*tag= d

FT /note= "Encodes protein which may be used as cleavable
 linker in the co-expression of multiple proteins"

XX WO200011196-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002720.

XX 18-AUG-1999; 98GB-00018003.

XX (ZENE) ZENECA LTD.

XX Evans IJ, Ray JA;

XX WPI; 2000-237658/20.

XX P-PSDB; AAY70314.

XX Polynucleotide sequences and expression products useful for producing
 PT transgenic plants that are resistant to microbial infections.

XX Claim 1; Fig 3; 77pp; English.

XX The present sequence is a Dahlia merckii cDNA encoding an antimicrobial
 CC preproprotein Dm2.5. This sequence is useful in the production of
 CC transgenic plants which show improved resistance to infections by
 CC microorganisms such as bacteria and fungi. Transgenic plants include e.g.
 CC field crops, fruits and vegetables, such as canola, sunflower, tomato,
 CC apple, banana, pear and mango

XX Sequence 577 BP; 178 A; 96 C; 140 G; 163 T; 0 U; 0 Other;

Query Match

Best Local Similarity 39.7%; Score 177.2; DB 3; Length 577;

Matches 234; Conservative 0; Mismatches 28; Indels 30; Gaps 1;

QY 155 AGATATCCATCCGTTAGTGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
 DB 82 AGATATCAACAGTGTGAGAGGAGAGTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 141
 QY 215 CTGTGGCAATACGGGACACTTGTGCAACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
 DB 142 CTGTGGCAACACGGGACACTGTGACNACCATGTAAATATCTGGGAGGGGGCGCCCATGG 201
 QY 275 AGCGTGTCATGTGCGTAAACCGGAAACACATGTGTTTCTGTACTTTCAATTGTAAAGAGC 334
 DB 202 GCGGTGCCACGTCGTGGAGGAAACACATGTGTTTCTGTACTTTCAAGTGTCCCAAGC 261
 QY 335 CGAAGAGCTTGCTCAAGCAAACTTAAGCCGAAACACTCGCTCAAGCAAACTTAATGC 394
 DB 262 CGAAAAGCTT-----GCTCAAGCAAAAGTTAATGC 291
 QY 395 CCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTCCAAACGTTGAACATCCG 446
 DB 292 CCAAGAGCTTGACCGTGATGCCAAGAAAGTGGTCCGAAAGTGAATCCGAAACATCCG 343

RESULT 11

AAZ99333

ID AAZ99333 standard; DNA; 485 BP.

XX AAZ99333;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.

XX Synthetic.

XX Dahlia merckii.

XX Unidentified.

XX Key Location/Qualifiers
 FH CDS 3..476

FT /*tag= a

FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1999; 98GB-00018001.

XX 04-DEC-1999; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84066.

XX Improving expression of polyproteins in plants involves coexpression of
 PT two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 28; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 CC (AMP) 1 and the antifungal protein 2 (APF2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide

| | | | | | | | | | | |
|----|--|---|--------------|--------------|------------|--------|--------|----------|------|----|
| CC | comprising a cleavage site, whereby the expressed polypeptide is post- | | | | | | | | | |
| CC | translationally processed into the component protein molecules. The | | | | | | | | | |
| CC | propeptide sequence is rich in amino acids A, V, S and T and contains | | | | | | | | | |
| CC | dipeptidic sequences consisting of either two acidic, two basic or one | | | | | | | | | |
| CC | acidic and one basic residue as a cleavable linker sequence | | | | | | | | | |
| XX | | | | | | | | | | |
| SQ | Sequence | 485 BP; | 124 A; | 107 C; | 128 G; | 126 T; | 0 U; | 0 Other; | | |
| | Query Match | 38.8%; | Score | 173.2; | DB | 3; | Length | 485; | | |
| | Best Local Similarity | 85.1%; | Pred. | No. 1.5e-37; | | | | | | |
| | Matches | 206; | Conservative | 0; | Mismatches | 33; | Indels | 3; | Gaps | 1; |
| QY | 155 | AGATATCGATCCGTTAGTGTGAGAACTATCGGAGAAAGCTAGCAAGACATGTCGGGAAA | 214 | | | | | | | |
| Db | 65 | AGATATCGATCCGTTAGTGTGAGAACTATCGGAGAAAGCTAGCAAGACATGTCGGGCAA | 124 | | | | | | | |
| QY | 215 | CTGTGGCAATACGGGACATTTGTGACACCACTTAATCATCGGAGGTTCGGCCCATGG | 274 | | | | | | | |
| Db | 125 | CTGTGGCAACACGGGACATTTGTGACACCACTTAATCATCGGAGGTTCGGGCTCAGG | 184 | | | | | | | |
| QY | 275 | ACGCTGTCATTCGCTAACCGGAAACACATGTTTCTGTTACTTCAATTGTAATAAAGC | 334 | | | | | | | |
| Db | 185 | ACGCTGTCATTCGCTTAACCGGAAACACATGTTTCTGTTACTTCAATTGTCCTAAGC | 244 | | | | | | | |
| QY | 335 | CGAAAGCTTCTCAAGACAAACTTAAAG---CCGACAACTCGCTCAAGACAAACTTAA | 391 | | | | | | | |
| Db | 245 | TGAGGAGCTCTCTCTCTATTCTTCTGAAGAACTTGTCTCAAGAAAGAGCTCC | 304 | | | | | | | |
| QY | 392 | TG | 393 | | | | | | | |
| Db | 305 | TG | 306 | | | | | | | |

RESULT 12
AAZ99329
ID AAZ99329 standard; DNA; 446 BP.
XX
XX
AC AAZ99329;
AC
XX
XX
DT 03-JUL-2000 (first entry)
XX
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.

```

RESULT 12
AAZ99329
ID AAZ99329 standard; DNA; 446 BP.
XX
XX AAZ99329;
XX
XX 03-JUL-2000 (first entry)
XX
XX DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptid
XX protein expression; plant defensin; RsAFP2; antifungal protein;
XX
XX Synthetic.
XX Dahlia merckii.
XX Unidentified.
XX
Key Location/Qualifiers
CDS 3..437
/*tag= a
/product= "fusion protein of DmAMP1 and RsAFP2"
FT
FT

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| | |
|--|--|
| WO200011175-A1. | |
| 02-MAR-2000. | |
| 17-AUG-1999; | 99WO-GH002716. |
| 18-AUG-1998; | 98GB-00018001. |
| 04-DEC-1998; | 98GB-00026753. |
| (ZENE) ZENECA LTD. | |
| Broekaert WF, | Francois IEJA, De Bolle MFC, Evans IJ, Ray JA; |
| WPI; 2000-246564/21. | |
| P-PSDB; AAY84062. | |
| Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit. | |

The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (AfF2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence

Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other:

| Query Match | 38.6%; | Score 172.2; | DB 3; | Length 446; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 93.3%; | Pred. No. 2.7e-37; | | |
| Matches 180; | Conservative 0; | Mismatches 13; | Indels 0; | Gaps 0 |
| Oy | 155 | AGATATCGCATCCGTTAGTGGAGACACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA | 214 | |
| | | | | |
| Db | 65 | AGATATCGCATCCGTTAGTGGAGACACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA | 124 | |
| | | | | |
| Oy | 215 | CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGGAGGGTGGCGGCCCATGG | 274 | |
| | | | | |
| Db | 125 | CTGTGGCAACACGGGACATTTGTGCAACCAATGTAAATCATGGAGGGTGGCGGTCACGG | 184 | |
| | | | | |
| Oy | 275 | ACGGTGTCTATGTGCTACCGGGAACACATGTTTCTGTACTTCAATTGTAAAAAAGC | 334 | |
| | | | | |
| Db | 185 | ACGGTGTCTATGTGCTGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAACGCGC | 244 | |
| | | | | |
| Oy | 335 | CGAAAGACTTGCT | 347 | |
| | | | | |
| Db | 245 | CGACGAGGTGGCT | 257 | |
| | | | | |

| | |
|----------|---|
| RESULT | 13 |
| AAZ99334 | |
| ID | AAZ99334 standard; DNA; 1093 Bp. |
| XX | |
| AC | AAZ99334; |
| XX | |
| DT | 03-JUL-2000 (first entry) |
| DE | DNA encoding a fusion protein of DmAMP1, RsAPP2, HsAPP1 and AceAMP1. |
| XX | |
| KW | Antimicrobial protein; AMP1; transgenic plant; linker propeptide; |
| KX | protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss. |
| XX | |
| OS | Synthetic. |
| OS | Dahlia merckii. |
| OS | Unidentified. |
| XX | |
| FH | Key |
| CDS | Location/Qualifiers 3..1085 /*tag= a /product= "fusion protein of plant defensins" |
| FT | |
| FT | |
| PN | WO200011175-A1. |
| PD | |
| PD | 02-MAR-2000. |
| PP | 17-AUG-1999; 99WO-GB002716. |
| XX | |
| PR | 18-AUG-1998; 98GB-00018001. |
| PR | 04-DEC-1998; 98GB-00026753. |
| XX | |
| PA | (ZENECA) ZENECA LTD. |

| | | |
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| XX | WO200011175-A1. | 99WO-GB002716. |
| PN | | |
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| XX | | |
| XX | 02-MAR-2000. | |
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| XX | | |
| XX | | |
| XX | 17-AUG-1999; | 99WO-GB002716. |
| XX | | |
| XX | 18-AUG-1998; | 98GB-00018001. |
| PR | | |
| PR | 04-DEC-1998; | 98GB-00026753. |
| XX | | |
| XX | (ZENE) ZENECA LTD. | |


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XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX PT P-PSDB; AAY84067.
XX XX
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Disclosure; Fig 29; 151pp; English.
XX CC
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1, antifungal protein 2 (RaFP2), HsAFP1 and AceAMP1, linked by
XX CC linker propeptides of the invention. The specification describes methods
XX CC for improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX CC
XX CC Sequence 1093 BP; 278 A; 271 C; 287 G; 257 T; 0 U; 0 Other;
XX CC
XX CC Query Match 38.1%; Score 170; DB 3; Length 1093;
XX CC Best Local Similarity 84.3%; Pred. No. 1.5e-36;
XX CC Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
XX CC
XX CC QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
XX CC |||||
XX CC Db 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 124
XX CC |||||
XX CC QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
XX CC |||||
XX CC Db 125 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 184
XX CC |||||
XX CC QY 275 AGCGTGTCTATGTCGCTTAATCGGGAACACATGTTTCTGTACTTCAATTTGAAAAGC 334
XX CC |||||
XX CC Db 185 AGCGTGTCTATGTCGCTTAATCGGGAACACATGTTTCTGTACTTCAATTTGAAAAGC 244
XX CC |||||
XX CC QY 335 CQAAAGCTTGTCTAAGACAACTTAAG---CCGAAACATTCGCTCAAGACAACTTAA 391
XX CC |||||
XX CC Db 245 TGAGGAAGCTGCTGCTGCTATTCTCTGAAGCTTCTGAAGAACTTGCTCAAGAGAACTCC 304
XX CC |||||
XX CC QY 392 TG 393
XX CC ||
XX CC Db 305 TG 306
XX CC
XX CC RESULT 14
XX CC ID AAZ99324 standard; DNA; 522 BP.
XX CC AC AAZ99324;
XX CC XX
XX CC DT 03-JUL-2000 (first entry)
XX CC DE DNA encoding a fusion protein of DmAMP1 and RaFP2.
XX CC KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX CC KW protein expression; plant defensin; RaFP2; antifungal protein; AFP2; ss.
XX CC OS Synthetic.
XX CC OS Dahlia merckii.
XX CC OS Unidentified.
XX CC FH Key Location/Qualifiers
XX CC FT misc_feature 160..309
XX CC /*tag= a
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FT misc_feature /note= "encodes DmAMP1"
FT 358..510
FT /*tag= b
FT /note= "encodes RaFP2"
XX PN WO200011175-A1.
XX XX
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX XX (ZENE ) ZENECA LTD.
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX PT P-PSDB; AAY84057.
XX XX
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 8; 151pp; English.
XX CC
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX CC
XX CC Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
XX CC
XX CC Query Match 37.9%; Score 169.2; DB 3; Length 522;
XX CC Best Local Similarity 95.6%; Pred. No. 1.9e-36;
XX CC Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX CC
XX CC QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
XX CC |||||
XX CC Db 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197
XX CC |||||
XX CC QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
XX CC |||||
XX CC Db 198 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 257
XX CC |||||
XX CC QY 275 AGCGTGTCTATGTCGCTTAATCGGGAACACATGTTTCTGTACTTCAATTTGAAAAGC 334
XX CC |||||
XX CC Db 258 AGCGTGTCTATGTCGCTTAATCGGGAACACATGTTTCTGTACTTCAATTTGAAAAGC 317
XX CC |||||
XX CC QY 335 CG 336
XX CC ||
XX CC Db 318 TG 319
XX CC
XX CC RESULT 15
XX CC ID AAZ54387
XX CC XX AAZ54387 standard; DNA; 460 BP.
XX CC AC AAZ54387;
XX CC XX
XX CC DT 11-APR-2001 (first entry)
XX CC DE Plant defensin coding sequence.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 12:55:37 ; Search time 136 Seconds
(without alignments)
5366.025 Million cell updates/sec

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Perfect score: 446
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 819138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 154.2 | 34.6 | 565 | 4 | US-09-589-733C-6 |
| 2 | 99.4 | 22.3 | 150 | 1 | US-08-377-687-31 |
| 3 | 99.4 | 22.3 | 150 | 1 | US-08-777-192-31 |
| 4 | 99.4 | 22.3 | 150 | 3 | US-08-971-982-31 |
| 5 | 91.4 | 20.5 | 150 | 1 | US-08-377-687-33 |
| 6 | 91.4 | 20.5 | 150 | 1 | US-08-777-192-33 |
| 7 | 91.4 | 20.5 | 150 | 3 | US-08-971-982-33 |
| 8 | 86.6 | 19.4 | 150 | 1 | US-08-377-687-34 |
| 9 | 86.6 | 19.4 | 150 | 1 | US-08-777-192-34 |
| 10 | 86.6 | 19.4 | 150 | 3 | US-08-971-982-34 |
| 11 | 58.4 | 13.1 | 147 | 1 | US-08-377-687-36 |
| 12 | 58.4 | 13.1 | 147 | 1 | US-08-777-192-36 |
| 13 | 58.4 | 13.1 | 147 | 3 | US-08-971-982-36 |
| 14 | 44.6 | 10.0 | 270 | 1 | US-08-627-706-14 |
| 15 | 44.6 | 10.0 | 270 | 3 | US-09-103-489-14 |
| 16 | 44.6 | 10.0 | 270 | 4 | US-09-829-381D-14 |
| 17 | 44.6 | 10.0 | 286 | 1 | US-08-627-706-12 |
| 18 | 44.6 | 10.0 | 286 | 3 | US-09-103-489-12 |
| 19 | 44.6 | 10.0 | 286 | 4 | US-09-829-381D-12 |
| 20 | 40.8 | 9.1 | 500 | 1 | US-08-627-706-9 |
| 21 | 40.8 | 9.1 | 500 | 3 | US-09-103-489-9 |
| 22 | 40.8 | 9.1 | 500 | 4 | US-09-829-381D-9 |
| 23 | 40.8 | 9.0 | 414 | 1 | US-08-377-687-48 |
| 24 | 40.8 | 9.0 | 414 | 1 | US-08-777-192-48 |
| 25 | 40.8 | 9.0 | 414 | 3 | US-08-971-982-48 |
| 26 | 40.8 | 9.0 | 414 | 3 | US-09-077-951-19 |
| 27 | 40.8 | 9.0 | 414 | 4 | US-09-077-948A-45 |

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| 28 | 39 | 8.7 | 288 | 1 | US-08-377-687-58 | Sequence 58, Appl |
| 29 | 39 | 8.7 | 288 | 1 | US-08-777-192-58 | Sequence 58, Appl |
| 30 | 39 | 8.7 | 288 | 3 | US-08-971-982-58 | Sequence 58, Appl |
| C 31 | 38.8 | 8.7 | 112 | 4 | US-09-589-733C-32 | Sequence 32, Appl |
| C 32 | 38.6 | 8.7 | 7218 | 1 | US-08-232-463-14 | Sequence 14, Appl |
| 33 | 38.4 | 8.6 | 1346 | 4 | US-09-589-733C-9 | Sequence 9, Appl |
| 34 | 38.2 | 8.6 | 60 | 1 | US-08-377-687-32 | Sequence 32, Appl |
| 35 | 38.2 | 8.6 | 60 | 1 | US-08-777-192-32 | Sequence 32, Appl |
| 36 | 38.2 | 8.6 | 60 | 3 | US-08-971-982-32 | Sequence 32, Appl |
| C 37 | 37.4 | 8.4 | 1141 | 4 | US-09-806-708B-32 | Sequence 22, Appl |
| C 38 | 35.2 | 7.9 | 601 | 4 | US-09-949-016-154963 | Sequence 154963, |
| C 39 | 35.2 | 7.9 | 601 | 4 | US-09-949-016-178474 | Sequence 178474, |
| C 40 | 35.2 | 7.9 | 942 | 4 | US-09-270-767-3330 | Sequence 3330, Ap |
| C 41 | 35.2 | 7.9 | 942 | 4 | US-09-270-767-18612 | Sequence 18612, A |
| C 42 | 35.2 | 7.9 | 99830 | 4 | US-09-949-016-16859 | Sequence 16859, A |
| C 43 | 35.2 | 7.9 | 385136 | 4 | US-09-949-016-16073 | Sequence 16073, A |
| C 44 | 35 | 7.8 | 51835 | 4 | US-09-949-016-17101 | Sequence 17101, A |
| 45 | 35 | 7.8 | 52032 | 4 | US-09-949-016-11789 | Sequence 11789, A |

ALIGNMENTS

RESULT 1
US-09-589-733C-6
; Sequence 6, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Craata, Oswald R.
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09589,733C
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-09-589-733C-6

| | | | | |
|-----------------------|--------------|--|----------------|-------------|
| Query Match | 34.6% | Score 154.2; | DB 4; | Length 565; |
| Best Local Similarity | 76.5% | Pred. No. 8.6e-38; | | |
| Matches 189; | Conservative | 0; | Mismatches 58; | Indels 0; |
| Gaps | 0; | | | |
| QY | 155 | AGATATCCATCCGTTAGTGGAGAACTATGGAGAAAGCTAGCAAGACATGTCGGGAAA | 214 | |
| DB | 99 | AGAAATCGATCGGTGAAAGGAGATTATGTGAGAGGCGAGCCAGACATGTCGGGAA | 158 | |
| QY | 215 | CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCCATGG | 274 | |
| DB | 159 | ATGTGGCAAGACAAACACTGTGATGACCACTGTGCAAGTCTTGGAGGGTGGAGCCCATGG | 218 | |
| QY | 275 | AGCGTGTGATGTCGTAACGGGAAAACACATGTTTCTGTACTTCAATTTGTAATAAAGC | 334 | |
| DB | 219 | AGCTTGTGATGTCGTAACGGGAAAACACATGTTTCTGTACTTCAATTTGTAATAAAGC | 278 | |
| QY | 335 | CGAAAGCTTGTCTAAGCAAACTTAAAGCCGAAACACTCGCTCAAGCAAACTTAATGC | 394 | |
| DB | 279 | CCAGAAAGTGGTCTAGGATAAACTCAGAGCGGAGAGCTCGCCAGGAGAGATTGAACC | 338 | |
| QY | 395 | CCAAAAG 401 | | |
| DB | 339 | CGAAAAG 345 | | |

```
RESULT 2
US-08-377-687-31
; Sequence 31, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-377-687-31

; Query Match 22.3%; Score 99.4; DB 1; Length 150;
; Best Local Similarity 79.2%; Pred. No. 4.6e-21;
; Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACATATCGGAAAGCTAGCAACATGTCGGGAACTGTGGCAATACGGGACATTGT 236
Db 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTCGGAAACACTGGGACATTGC 60

Qy 237 GACACCAATGTAATCATGCGGGTGGCGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
Db 61 GATACCAATGCAAGTCTTGGAGGAGCTGCTCATGAGCTTGCCATGTTAGAACGGA 120

Qy 297 AAACACATGTGTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 3
US-08-777-192-31
; Sequence 31, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
```

```
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-777-192-31

; Query Match 22.3%; Score 99.4; DB 1; Length 150;
; Best Local Similarity 79.2%; Pred. No. 4.6e-21;
; Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACATATCGGAAAGCTAGCAACATGTCGGGAACTGTGGCAATACGGGACATTGT 236
Db 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTCGGAAACACTGGGACATTGC 60

Qy 237 GACACCAATGTAATCATGCGGGTGGCGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
Db 61 GATACCAATGCAAGTCTTGGAGGAGCTGCTCATGAGCTTGCCATGTTAGAACGGA 120

Qy 297 AAACACATGTGTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 4
US-08-971-982-31
; Sequence 31, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
```

Query Match 20.5%; Score 91.4; DB 1; Length 150;
Best Local Similarity 75.8%; Pred. No. 1.4e-18;
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

[illegible]

RESULT 6
US-08-777-192-33
; Sequence 33, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUR, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B. R.G.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-777-192-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;
Best Local Similarity 75.8%; Pred. No. 1.4e-18;
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0

Qy 177 GAACATATCGGAGAACTAGCAACACATGTCGGGAACCTGTGCGCAATACGGGACATTGT 236
Db 1 GAGCTTTGGGAGAGCTTCTTAAGACTTGTGCTGGAAACTGCGGAAACACTAAGCATTTGC 60

Qy 237 GAACAACCAATGTAAATCATGCGAGGGGTGCGGCCCATGGAGCGGTGTCATGTGCGTAAACGGG 296
Db 61 GATGATCAATGCAAGTCTTTGGAGGGAGCTGCTCATGGAGCTTGCATGTTAGAAACCGA 120

Qy 297 AAACACATGTGTTTCTGTACTTCAATTG 325
Db 121 AAGCATATGTGTTCTGTACTTCAACTG 149

```

RESULT 7
US-08-971-982-33
; Sequence 33, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:

| | |
|---|--|
| TELEPHONE: 202-861-3000 | |
| TELEFAX: 202-822-0944 | |
| INFORMATION FOR SEQ ID NO: 33: | |
| SEQUENCE CHARACTERISTICS: | |
| LENGTH: 150 base pairs | |
| TYPE: nucleic acid | |
| STRANDEDNESS: both | |
| TOPOLOGY: linear | |
| MOLECULE TYPE: CDNA | |
| SEQUENCE DESCRIPTION: SEQ ID NO: 33: | |
| US-08-971-982-33 | |
| Query Match | 20.5%; Score 91.4; DB 3; Length 150; |
| Best Local Similarity | 75.8%; Pred. No. 1.4e-18; |
| Matches 113; Conservative | 0; Mismatches 36; Indels 0; Gaps 0 |
| Qy | 177 GAACATATGCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTGT 236 |
| Db | 1 GAGCTTTGCGAGAGGCTTCTAAGACTTGTCTGGAACTCGCGAAACACTTAAGCATTGC 60 |
| Qy | 237 GACAACCAATGTAATCATATGCGAGGTCGGGCCCATGAGCGGTGTCATGTGCGTAACGGG 296 |
| Db | 61 GATGATCAATGCAAGTCTTTGGGAGGAGCTGCTCATGGAGCTTGCCATGTTAGAAACGGA 120 |
| Qy | 297 AAACACATGTTCTTCTGTACTTCAATTG 325 |
| Db | 121 AAGCATATGCTTCTGTACTTCAACTG 149 |
| RESULT 8 | |
| US-08-377-687-34 | |
| Sequence 34, Application US/08377687 | |
| Patent No. 5536525 | |
| GENERAL INFORMATION: | |
| APPLICANT: BROEKERT, WILLEM F. | |
| APPLICANT: CAMMUE, BRUNO P.A. | |
| APPLICANT: OSBORN, RUPERT W. | |
| APPLICANT: REES, SARAH B. | |
| APPLICANT: TERRAS, FRANKY R.G. | |
| APPLICANT: VANDERLEIDEN, JOZEF | |
| TITLE OF INVENTION: BIOCIDAL PROTEINS | |
| NUMBER OF SEQUENCES: 59 | |
| CORRESPONDENCE ADDRESS: | |
| ADDRESSEE: CUSHMAN DARBY & CUSHMAN | |
| STREET: 1100 NEW YORK AVENUE, N.W. | |
| CITY: WASHINGTON | |
| STATE: D.C. | |
| COUNTRY: USA | |
| ZIP: 20005 | |
| COMPUTER READABLE FORM: | |
| MEDIUM TYPE: Floppy disk | |
| COMPUTER: IBM PC compatible | |
| OPERATING SYSTEM: PC-DOS/MS-DOS | |
| SOFTWARE: Patent in Release #1.0, Version #1.25 | |
| CURRENT APPLICATION DATA: | |
| APPLICATION NUMBER: US/08/377,687 | |
| FILING DATE: | |
| CLASSIFICATION: 800 | |
| PRIOR APPLICATION DATA: | |
| APPLICATION NUMBER: US 08/002,480 | |
| FILING DATE: 04-JAN-1993 | |
| ATTORNEY/AGENT INFORMATION: | |
| NAME: KOKULIS, PAUL N. | |
| REGISTRATION NUMBER: 16,773 | |
| REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A | |
| TELECOMMUNICATION INFORMATION: | |
| TELEPHONE: 202-861-3000 | |
| TELEFAX: 202-822-0944 | |
| INFORMATION FOR SEQ ID NO: 34: | |
| SEQUENCE CHARACTERISTICS: | |
| LENGTH: 150 base pairs | |
| TYPE: nucleic acid | |
| STRANDEDNESS: both | |

TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-377-687-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTCGGAAACTGTGGCAATACGGACATTGT 236
DB 1 GAGCTTTGCGAGAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAAATCATGAGGAGGTGCGGCCCATGGAGCGTGTCTATGCGTAAACGGG 296
DB 61 GATACAACTGCAAGCTCTTGGAGGAGGAGTGTCTCATGGAGCTTGCCATGTTAGATCTGGA 120

QY 297 AAACACATGTGTTCTCTGTTACTTCAATTG 325
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 9
US-08-777-192-34
Sequence 34, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-JAN-1993
APPLICATION NUMBER: US 08/777,192
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-777-192-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTCGGAAACTGTGGCAATACGGACATTGT 236
DB 1 GAGCTTTGCGAGAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAAATCATGAGGAGGTGCGGCCCATGGAGCGTGTCTATGCGTAAACGGG 296
DB 61 GATACAACTGCAAGCTCTTGGAGGAGGAGTGTCTCATGGAGCTTGCCATGTTAGATCTGGA 120

QY 297 AAACACATGTGTTCTCTGTTACTTCAATTG 325
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 10
US-08-971-982-34
Sequence 34, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US/08/971,982
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-971-982-34

Query Match 19.4%; Score 86.6; DB 3; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTCGGAAACTGTGGCAATACGGACATTGT 236
DB 1 GAGCTTTGCGAGAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAAATCATGAGGAGGTGCGGCCCATGGAGCGTGTCTATGCGTAAACGGG 296
DB 61 GATACAACTGCAAGCTCTTGGAGGAGGAGTGTCTCATGGAGCTTGCCATGTTAGATCTGGA 120

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Qy 297 AACACATGTGTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGTGCTTCTGCTACTTCACTG 149

RESULT 11
US-08-377-687-36
; Sequence 36, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377.687
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002.480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-377-687-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;
Best Local Similarity 66.9%; Pred. No. 2.5e-08;
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

Qy 178 AACTATCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTGTG 237
Db 2 ACCTTTGGAGAGAGCTTCTTACTTGAGATGGAACTGGGAAACACTGGACATTGCG 61

Qy 238 ACAACCAATGTAATCATGAGAGGTCGGGCCCATGGAGCGTGTCTATGTCGTTAACGGGA 297
Db 62 ATACTCAATCGAGAAACTGGGAGTCTGCTAAGCATGGAGCTTGCCATAAG---AGAGGAA 118

Qy 298 AACACATGTTCTGTTACTTCAATTG 325
Db 119 ACTGGAAGTCTTCTGCTACTTCGATTG 146

RESULT 12
US-08-777-192-36
; Sequence 36, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.

; Sequence 36, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777.192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002.480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-777-192-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;
Best Local Similarity 66.9%; Pred. No. 2.5e-08;
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

Qy 178 AACTATCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTGTG 237
Db 2 ACCTTTGGAGAGAGCTTCTTACTTGAGATGGAACTGGGAAACACTGGACATTGCG 61

Qy 238 ACAACCAATGTAATCATGAGAGGTCGGGCCCATGGAGCGTGTCTATGTCGTTAACGGGA 297
Db 62 ATACTCAATCGAGAAACTGGGAGTCTGCTAAGCATGGAGCTTGCCATAAG---AGAGGAA 118

Qy 298 AACACATGTTCTGTTACTTCAATTG 325
Db 119 ACTGGAAGTCTTCTGCTACTTCGATTG 146

RESULT 13
US-08-971-982-36
; Sequence 36, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
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VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARB & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187504-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-08-971-982-36

Query Match 13.1%; Score 58.4; DB 3; Length 147;
Best Local Similarity 66.9%; Pred. No. 2.5e-08;
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
QY 178 AACTATGCGAGAACTAGCAGACATGTCGGGAACTGTGGCAATACGGACATTGTG 237
Db 2 ACCITTCGAGAGAGCTTCTTACTTGGACTGGAACTGCGGAAACACTGGACATTGCG 61
QY 238 ACAACCAATGTAATCATGGGGGGTGGCCCATGAGCGTGTCTATGCGTAACGGGA 297
Db 62 ATACTCAATGCAAGAACTGGGAGTCTGCTAAGCATGGAGCTTGCCATAAG---AGAGGAA 118
QY 298 AACACATGTGTTCTGTACTTCAATTG 325
Db 119 ACTGGAAGTGCTCTGCTACTTCGATTG 146

RESULT 14
US-08-627-706-14
; Sequence 14, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri

COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-14
Query Match 10.0%; Score 44.6; DB 1; Length 270;
Best Local Similarity 53.8%; Pred. No. 0.00065;
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 163 CATCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCA 222
Db 95 CAATGGTGGATGCCAAGGTTGTGCGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGA 154
QY 223 ATACGGGACATTGTGACAACTGTAATCATGGGAGGGTGGCCCATGAGCGTGPC 282
Db 155 ACAACATGTCATGCGAGAACTGCAAACTTGAAGAGAGCAACACGANTTTGCA 214
QY 283 ATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAG 333
Db 215 ACTATGTTCCAGCTCACAANTGATTGTTACTTCCCATGTTAATAG 265

RESULT 15
US-09-103-489-14
; Sequence 14, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

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; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-489-14

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Query Match      10.0%; Score 44.6; DB 3; Length 270;
Best Local Similarity 53.8%; Pred. No. 0.00065;
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 163 CATCCGTTAGTGGAGAACTATCGAGAAAGCTAGCAAGACATGGTCGGGAAACTGTGGCA 222
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 223 ATACGGGACATGTGCACACCAATGTAATCATGGAGGGTCCGGCCCATGGAGCGTGTG 282
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 ACAACAATGCATGCAGGAAACCAATCGAACCCTTTGAAAGAGACAGACACGGATCTTGCA 214
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 283 ATGTGCGTAACGGGAAACACACATGTGTTCTGTCTTCAATTGTAATAAAG 333
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 ACTATGTCTTCCAGCTCACAATGTAATTTGTTACTTCCCATGTTAATAAG 265
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: March 18, 2005, 16:31:56
Job time : 137 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 14:31:06 ; Search time 420 Seconds

(without alignments)
6321.756 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atggtgaatcgttggtgc.....ttccaaacgttgaaacatccg 446

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 209.4 | 47.0 | 529 | 15 | US-10-178-449A-48 |
| 2 | 203 | 45.5 | 579 | 15 | US-10-178-449A-31 |
| 3 | 168.6 | 37.8 | 460 | 15 | US-10-178-449A-3 |
| 4 | 168.6 | 37.8 | 503 | 15 | US-10-178-449A-1 |
| 5 | 161 | 36.1 | 461 | 15 | US-10-178-449A-46 |
| 6 | 156.4 | 35.1 | 457 | 15 | US-10-178-449A-13 |
| 7 | 156.4 | 35.1 | 463 | 15 | US-10-178-449A-9 |
| 8 | 156.4 | 35.1 | 603 | 15 | US-10-178-449A-11 |
| 9 | 154.8 | 34.7 | 458 | 15 | US-10-178-449A-21 |
| 10 | 154.8 | 34.7 | 460 | 15 | US-10-178-449A-17 |
| 11 | 154.2 | 34.6 | 565 | 17 | US-10-636-396-6 |
| | | | | | Sequence 48, Appl |
| | | | | | Sequence 31, Appl |
| | | | | | Sequence 3, Appl |
| | | | | | Sequence 1, Appl |
| | | | | | Sequence 46, Appl |
| | | | | | Sequence 13, Appl |
| | | | | | Sequence 9, Appl |
| | | | | | Sequence 11, Appl |
| | | | | | Sequence 21, Appl |
| | | | | | Sequence 17, Appl |
| | | | | | Sequence 6, Appl |

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|----|-------|------|---------|----|---------------------|
| 12 | 154.2 | 34.6 | 565 | 18 | US-10-636-026-6 |
| 13 | 153.2 | 34.3 | 464 | 15 | US-10-178-449A-19 |
| 14 | 153.2 | 34.3 | 472 | 15 | US-10-178-449A-23 |
| 15 | 138.4 | 31.0 | 439 | 15 | US-10-178-449A-15 |
| 16 | 99.4 | 22.3 | 150 | 9 | US-09-759-584-31 |
| 17 | 91.4 | 20.5 | 150 | 9 | US-09-759-584-33 |
| 18 | 88.2 | 19.8 | 610 | 15 | US-10-178-449A-29 |
| 19 | 88.2 | 19.8 | 658 | 15 | US-10-178-449A-34 |
| 20 | 87.8 | 19.7 | 156 | 15 | US-10-178-449A-34 |
| 21 | 86.6 | 19.4 | 150 | 9 | US-09-759-584-34 |
| 22 | 85.8 | 19.2 | 501 | 15 | US-10-178-449A-5 |
| 23 | 74.8 | 16.8 | 250 | 15 | US-10-178-449A-36 |
| 24 | 65.8 | 14.8 | 373 | 9 | US-09-770-696-283 |
| 25 | 58.4 | 13.1 | 147 | 9 | US-09-759-584-35 |
| 26 | 56.6 | 12.7 | 470 | 14 | US-10-178-213-88 |
| 27 | 47.8 | 10.7 | 499 | 15 | US-10-178-449A-25 |
| 28 | 47.8 | 10.7 | 517 | 15 | US-10-178-449A-27 |
| 29 | 44.6 | 10.0 | 270 | 9 | US-09-829-381A-14 |
| 30 | 44.6 | 10.0 | 270 | 17 | US-10-681-972-14 |
| 31 | 44.6 | 10.0 | 286 | 9 | US-09-829-381A-12 |
| 32 | 44.6 | 10.0 | 286 | 17 | US-10-681-972-12 |
| 33 | 41.6 | 9.3 | 1616 | 9 | US-09-732-561-21 |
| 34 | 41.2 | 9.2 | 400 | 9 | US-09-732-561-15 |
| 35 | 40.8 | 9.1 | 500 | 9 | US-09-829-381A-9 |
| 36 | 40.8 | 9.1 | 500 | 17 | US-10-681-972-9 |
| 37 | 40.2 | 9.0 | 243 | 9 | US-09-938-842A-2046 |
| 38 | 40.2 | 9.0 | 243 | 11 | US-09-938-842A-2046 |
| 39 | 40 | 9.0 | 414 | 9 | US-09-759-584-48 |
| 40 | 40 | 9.0 | 414 | 13 | US-10-006-252A-19 |
| 41 | 40 | 9.0 | 414 | 17 | US-10-388-361A-45 |
| 42 | 39.6 | 8.9 | 335913 | 10 | US-09-754-853A-2 |
| 43 | 39.6 | 8.9 | 335913 | 10 | US-09-754-853A-3 |
| 44 | 39.2 | 8.8 | 3673778 | 16 | US-10-312-841-1 |
| 45 | 39 | 8.7 | 288 | 9 | US-09-759-584-58 |

ALIGNMENTS

RESULT 1

US-10-178-449A-48
; Sequence 48, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prensall, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 480_515, 521, 529
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (25)....(372)
US-10-178-449A-48

Query Match      47.0%; Score 209.4; DB 15; Length 529;
Best Local Similarity 82.5%; Pred. No. 4.2e-48;
Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 78 AGAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAAAGCTAGCAAGACATGTCAGGCAA 137

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 274
DB 138 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAAAGTATGAGTGGAGGCTGAGCCCATGG 197

QY 275 ACGGTGTCTATGCGTAAACGGGAAACACATGTTCTTCTTACTTCAATTTGAAAAAGC 334
DB 198 AGCTTGTCTATGCGTGGAGGAAACACATGTCGTTTGTATTCAATTTGAAAAAGC 257

QY 335 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 394
DB 258 TGAATAAAGCTCGTCAAGATAGTAAAGCTGAAAGAGCTTGAAGAGCAAACTCAAGGC 317

QY 395 CAAAAGCTTGACCGTGTATGCGCAAGAAAGTGGTTCCTCAAAACGTTGAACATCC 445
DB 318 AGATAAGTTTGACCATGATGCAAAAGAGTAGTAGTACCAATGTGCAACATCC 368

RESULT 2
US-10-178-449A-31
; Sequence 31, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
US-10-178-449A-31

Query Match      45.5%; Score 203; DB 15; Length 579;
Best Local Similarity 81.1%; Pred. No. 2.7e-46;
Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 92 AGAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAGAGCTAGCAAGACATGTCAGGCAA 151

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 274
DB 152 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAAAGTATGAGTGGAGGCTGAGCCCATGG 211

QY 275 ACGGTGTCTATGCGTAAACGGGAAACACATGTCGTTTCTTACTTCAATTTGAAAAAGC 334
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Db 212 AGCTTGTCTATGCGTGGAGGAAACACATGTCGTTTGTCTTATTCAATTTGAAAAAGC 271
QY 335 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 394
DB 272 TGAATAAAGCTCGTCAAGATAGTAAAGCTGAAAGAGCTTGAAGAGCAAACTCAAGGC 331
QY 395 CAAAAGCTTGACCGTGTATGCGCAAGAAAGTGGTTCCTCAAAACGTTGAACATCC 445
DB 332 AGATAAGTTTGACCATGATGCAAAAGAGTAGTAGTACCAATGTGCAACATCC 382

RESULT 3
US-10-178-449A-3
; Sequence 3, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Dimorphotheca sinuata
US-10-178-449A-3

Query Match      37.8%; Score 168.6; DB 15; Length 460;
Best Local Similarity 81.6%; Pred. No. 1e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 87 AGAATCGGACCTGTGAGAAAGTGCATATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 146

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 274
DB 147 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAAAGTATGAGTGGAGGCTGAGCCCATGG 206

QY 275 ACGGTGTCTATGCGTAAACGGGAAACACATGTCGTTTCTTACTTCAATTTGAAAAAGC 334
DB 207 TGGTGTCTATGCGTGGGAAACACATGTCGTTTCTTACTTCAATTTGAAAAAGC 266

QY 335 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTAGCAAGACATGTCGGGAAA 393
DB 267 CGAAAAGCTTGCCCAAGACAACTCAACGCTGAAAAATTCGGCCGTGATGACGTTAAAG 325

RESULT 4
US-10-178-449A-1
; Sequence 1, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
```

APPLICANT: Miao, Guo-Hua
APPLICANT: Presnail, James K.
APPLICANT: Rafalski, Jan antoni
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 503
TYPE: DNA
ORGANISM: Dimorphotheca sinuata
FEATURE:
NAME/KEY: misc feature
LOCATION: 321, 349, 416, 458, 474, 479, 482, 502
OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-1

Query Match 37.8%; Score 168.6; DB 15; Length 503;
Best Local Similarity 81.6%; Pred. No. 1.1e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 80 AGAAATCGCGACTGTGAGAAAGTGCATATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 139

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
DB 140 CTGTGGCAACACGGGACATGTGACGACCAGTGTAGTCTGGGAGAGCTGCAGCCCATGG 199

QY 275 AGCGTGTATGTGCGTAACGGGAAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 334
DB 200 TCGGTGTATGTGCGTGGTGGGAAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 259

QY 335 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATG 393
DB 260 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATG 318

RESULT 5
US-10-178-449A-46
Sequence 46, Application US/10178449A
Publication No. US20030140368A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert L.
APPLICANT: McCutchen, Billy Fred
APPLICANT: Miao, Guo-Hua
APPLICANT: Presnail, James K.
APPLICANT: Rafalski, Jan antoni
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46

LENGTH: 461
TYPE: DNA
ORGANISM: Helianthus annuus
FEATURE:
NAME/KEY: CDS
LOCATION: (14)...(340)
US-10-178-449A-46

Query Match 36.1%; Score 161; DB 15; Length 461;
Best Local Similarity 77.9%; Pred. No. 1.4e-34;
Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 76 AGAAATCGGATCGGTGAAGGGAGAAATATGTGAGAAAGCTAGCAAGACATGTCGGGAAA 135

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
DB 136 ATGTGGCAACACAGACACTGTGACGACCAGTGTGCAAGTCTTGGGAGGGTGCAGCCCATGG 195

QY 275 AGCGTGTATGTGCGTAACGGGAAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 334
DB 196 AGCTTGTACGTGCGCGTGGGAAAACACATGTGTTCTGTACTTCAACTGTTCCTCAAGC 255

QY 335 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATG 394
DB 256 CGAAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATG 315

QY 395 CGAAAAGCT 403
DB 316 CGAAAAGCT 324

RESULT 6
US-10-178-449A-13
Sequence 13, Application US/10178449A
Publication No. US20030140368A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert L.
APPLICANT: McCutchen, Billy Fred
APPLICANT: Miao, Guo-Hua
APPLICANT: Presnail, James K.
APPLICANT: Rafalski, Jan antoni
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 457
TYPE: DNA
ORGANISM: Parthenium argentatum Grey
FEATURE:
NAME/KEY: misc feature
LOCATION: 424...436
US-10-178-449A-13

Query Match 35.1%; Score 156.4; DB 15; Length 457;
Best Local Similarity 77.2%; Pred. No. 2.6e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGAAA 214

| | | | |
|----|-----|--|-----|
| Db | 91 | AGAAATCGGATCGGTGAAGGAGAACTATGTGAGARGCAAGCAAGACATGGTCTGGA | 150 |
| Qy | 215 | CTGTGGCAATACGGGACATTTGTGACAACCAATCATGGAGAGGTCGGGCCCATGG | 274 |
| Db | 151 | TTGTGTTAAACAAGACATTTGTGACGACCAATGCAAGTCTTGGGAGGTCACGCCCATGG | 210 |
| Qy | 275 | AGCGTGTCAATGTGCGTTACGGGAAACACATGTGTTCTGTACTTCAATTGTAANAAGC | 334 |
| Db | 211 | AGCTTGTCAATGTGCGCGGTGGGNAACACATGTGTTCTGTACTTCCAGTGCCCCAAGC | 270 |
| Qy | 335 | CGAAGAGCTTGCTCAAGACAACTTAAAGCGGAACAATCGCTCAAGACAAACTTAATGC | 394 |
| Db | 271 | CGAAGAAGATGGGCCAGGATAAACTCCGAGCTGAAAGAGCTTGCCAAGGAGAAGATTGAAGC | 330 |
| Qy | 395 | CCAAAA 400 | |
| Db | 331 | TGAAAA 336 | |

```

RESULT 7
US-10-178-449A-9
; Sequence 9, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; FILE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 413
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-9

```

| | Query Match | 35.1% | Score 156.4 | DB 15 | Length 463 |
|----|-----------------------|--|-------------------|----------|------------|
| | Best Local Similarity | 77.2% | Pred. No. 2.7e-33 | | |
| | Matches 190 | Conservative 0 | Mismatches 56 | Indels 0 | Gaps 0 |
| QY | 155 | AGATATCCGATCCGTTAGTGGAGAACTATCCGAGAAAGCTAGCAAGACATGTCGGGAAA | 214 | | |
| Db | 94 | AGAAATCGATCGTGAAGGGAGAACTATGTGAGAGGCAAGCAAGACATGTCCTGGAAA | 153 | | |
| QY | 215 | CTGTGGCAATACGGGACATTTGTGACACCAATCTAATCATCGGAGGGTGGCGCCATGG | 274 | | |
| Db | 154 | TTTGTTAAACAACAGACATTTGTGACGACCAATGCAAGTCTTGGAGGGTGCAGCCCATGG | 213 | | |
| QY | 275 | AGCGTGTCAATGTCGTAAACGGGAAAACATGTGTTTCTGTTACTTCAATTGTAAAAAAGC | 334 | | |
| Db | 214 | AGCTTGTCAATGTGCGCGGTGGGAAAACACATGTGTTCTTCTGTACTTCCAGTGCCCAAGC | 273 | | |
| QY | 335 | CGAAAGAGTTGCTCAAGACAAAACCTTAAAGCGCGAACAACTTCGCTCAAGACAAACTTAATGC | 394 | | |

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Db      274 CGAGAAGATGCCCCCAGGATAAACTCCGAGCTTGAAGAGCTTGCCAAAGAGAGAGATTGAAGC 333
Qy      395 CCAAAA 400
          ||||
Db      334 TGA AAAA 339

RESULT 8
US-10-178-449A-11
; Sequence 11, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herimann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
US-10-178-449A-11

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| | | | | |
|---|-----------------|---|-----------|-------------|
| Query Match | 35.1% | Score 156.4; | DB 15; | Length 603; |
| Best Local Similarity | 77.2%; | Pred. No. 3e-33; | | |
| Matches 190; | Conservative 0; | Mismatches 56; | Indels 0; | Gaps 0; |
| QY | 155 | AGATATCGCATCCGTTAGTGGAGAACTATCGGAGAAAGCTAGCAAGACATGGTCGGGAA | 214 | |
| | | | | |
| Db | 101 | AGAAATCGGATCGGTGAAGGAGAACTATGTGAAGGCAAGCAACATGGTCTGGAA | 160 | |
| | | | | |
| QY | 215 | CTGTGGCAATPACGGGCAATTGTGCACAAACCAATGTAAATCATATGGAGGGTGCGCCCATGG | 273 | |
| | | | | |
| Db | 161 | TTGTGTGTAAACACAAGACATTTGTGACGACCAATATGCAAGTCTTTGGAGGGTGCAGCCCATGG | 220 | |
| | | | | |
| QY | 275 | AGCGTGTCTATGTGCGTAAACGGGGAACACATGTCTTTCTGTACTTCAATTGTATAAAGC | 334 | |
| | | | | |
| Db | 221 | AGTTGTCTATGTGCGCGGTGGGAAACACATGTGCTTCTGTCTATTCAGATGCCCAAGC | 280 | |
| | | | | |
| QY | 335 | CGAAAAAGCTTGCTCAAGACAAACTTAAAGCCGAACAACTCGCTCAAGACAAACTTAATGC | 394 | |
| | | | | |
| Db | 281 | CGAAGAGATGGCCCGGATAAACTCCGAGCTGAAGAGCTTGCCAAAGGAGAAGATTGAAGC | 340 | |
| | | | | |
| QY | 395 | CCAAAA 400 | | |
| | | | | |
| Db | 341 | TGAAAA 346 | | |
| | | | | |
| RESULT 9 | | | | |
| US-10-178-449A-21 | | | | |
| ; Sequence 21, Application US/10178449A | | | | |
| ; Publication No. US20030140368A1 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Famodu, Omolayo O. | | | | |
| ; APPLICANT: Herrmann, Rafael | | | | |
| ; APPLICANT: Lu, Albert L. | | | | |
| ; APPLICANT: McCutchen, Billy Fred | | | | |
| ; APPLICANT: Miao, Guo-Hua | | | | |

```
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 322, 375, 402, 452
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-21

Query Match      34.7%; Score 154.8; DB 15; Length 458;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 72 AGAATCGGATCGGTGAGGAGAACTATGTGAGAGGCGCAAGACATGGTCGGAAA 131

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCGCCCATGG 274
Db 132 TTGTGGTAACACAGACACTGTGACGACCAATGCAAGTCTTGGAGGGTGCAGCCCATGG 191

QY 275 ACCGTGTCTATGTCGTAAACCGGAAACACATGTGTTCTGTACTTCAATTTAAAGAGC 334
Db 192 AGCTTGTCTATGTCGTGGGAGGAAACACATGTGTTCTGTACTTCCAGTGGCCCAAGC 251

QY 335 CGAAAGCTTGTCTCAAGCAAACTTTAAAGCCGAACTGCTCAAGCAAACTTAAATGC 394
Db 252 CGAGAAGATGGCCAGGATAAATCCGAGCTGAGAGCTTGCACAGAGAGATTGAAGC 311

QY 395 CCAAAA 400
Db 312 TGAATA 317

RESULT 10
US-10-178-449A-17
; Sequence 17, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07

; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 342
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-17

Query Match      34.7%; Score 154.8; DB 15; Length 460;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 89 AGAATCGGATCGGTGAGGAGAACTATGTGAGAGGCGCAAGACATGGTCGGAAA 148

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCGCCCATGG 274
Db 149 TTGTGGTAACACAGACACTGTGACGACCAATGCAAGTCTTGGAGGGTGCAGCCCATGG 208

QY 275 ACCGTGTCTATGTCGTAAACCGGAAACACATGTGTTCTGTACTTCAATTTAAAGAGC 334
Db 209 AGCTTGTCTATGTCGTGGGAGGAAACACATGTGTTCTGTACTTCCAGTGGCCCAAGC 268

QY 335 CGAAAGCTTGTCTCAAGCAAACTTTAAAGCCGAACTGCTCAAGCAAACTTAAATGC 394
Db 269 CGAGAAGATGGCCAGGATAAATCCGAGCTGAGAGCTTGCACAGAGAGATTGAAGC 328

QY 395 CCAAAA 400
Db 329 TGAATA 334

RESULT 11
US-10-636-396-6
; Sequence 6, Application US/10636396
; Publication No. US20040073971A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,396
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-6

Query Match      34.6%; Score 154.2; DB 17; Length 565;
Best Local Similarity 76.5%; Pred. No. 1.2e-32;
Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 99 AGAATCGGATCGGTGAGGAGAAATTTATGTGAGAGGCGCAAGCCAGACATGGTCCGGAAC 158
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; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 368
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-23

Query Match      34.3%; Score 153.2; DB 15; Length 472;
Best Local Similarity 76.4%; Pred. No. 2.1e-32;
Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 155 AGATATCCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 86 AGAAATCGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAAGACATGTCGGAAA 145

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAATCATGGGAGGGTGGGCCCATGG 274
Db 146 TTGTGTTAAACAAAGACATTTGTGACCAATGCAATGTCGGAGGGTGGAGCCCATGG 205

QY 275 AGCGTGTGATGTGCTTAAGCAAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 334
Db 266 CGAGAAGATGGCCCGAGGATTAACCTCCGAGCTGAAGAGCTTGCCCAAGGAGAGATTGAA 325

QY 395 CCAGAA 400
Db 326 TGAAGAA 331

RESULT 15
US-10-178-449A-15
; Sequence 15, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 439

; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 276, 288, 349, 438
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-15

Query Match      31.0%; Score 138.4; DB 15; Length 439;
Best Local Similarity 71.9%; Pred. No. 2.8e-28;
Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 155 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 93 AGAAATCGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAAGACATGTCGTGAAA 152

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAATCATGGGAGGGTGGGCCCATGG 274
Db 153 TTGTGTTAAACAAAGACATTTGTGACCAATGCAATGTCGGAGGGTGGAGCCCATGG 212

QY 275 AGCGTGTGATGTGCTTAAGCAAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 334
Db 213 AGCTTGTGATGTGCGCGGTGGGAAACACATGTCGCTTCTGCTACTTCCAGTGGCCCAAGC 272

QY 335 CGAAAAGCTTCTCAA -GACAAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 393
Db 273 CGAAGATGGCCCGAGGATTAACCTCCGAGCTGAAGAGCTTGCCCAAGGAGAGATTGAA 332

QY 394 CCCAAAAGCTTGACCGTGTGATGCCAAGA 420
Db 333 GCTGAAAAGAGCCGAGCAACCTTGA 359

Search completed: March 18, 2005, 19:33:33
Job time : 422 secs
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 18, 2005, 12:39:02 ; Search time 7103 Seconds
(without alignment)
2390.070 Million cell updates/sec

Title: US-09-763-019-5
Perfect score: 446
Sequence: 1 atggtgaatcggtcggttcg.....ttccaaacgttgaaacatccg 446

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gssi:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 198.6 | 44.5 | 604 | 5 | BQ989575 QGF18A17. |
| 2 | 197 | 44.2 | 616 | 5 | BQ984300 QGE21E24. |
| 3 | 197 | 44.2 | 620 | 5 | BQ984745 QGE4h04.Y |
| 4 | 197 | 44.2 | 641 | 5 | BU008575 QGH7E24.Y |
| 5 | 177.2 | 39.7 | 547 | 5 | BQ995419 QGF9P04.Y |
| 6 | 160.6 | 36.0 | 468 | 1 | AJ412176 AJ412176 |
| 7 | 154.2 | 34.6 | 606 | 6 | CD846862 DH0AB512E |
| 8 | 153.6 | 34.4 | 475 | 1 | AJ541276 AJ541276 |
| 9 | 131.2 | 29.4 | 239 | 5 | BQ844100 QCA12M13. |
| 10 | 127 | 28.5 | 359 | 1 | AJ541406 AJ541406 |
| 11 | 127 | 28.5 | 420 | 1 | AJ541283 AJ541283 |
| 12 | 123.6 | 27.7 | 603 | 5 | BQ847005 QGA20O20. |
| 13 | 122 | 27.4 | 447 | 1 | AJ306450 AJ306450 |
| 14 | 100.2 | 22.5 | 487 | 1 | AJ412470 AJ412470 |
| 15 | 94 | 21.1 | 340 | 5 | BQ845488 QGA16N20. |
| 16 | 94 | 21.1 | 341 | 5 | BQ861273 QGC18A12. |
| 17 | 77.6 | 17.4 | 605 | 5 | BU011479 QGJ16F16. |
| 18 | 76 | 17.0 | 594 | 5 | BU014657 QGJ7P01.Y |
| 19 | 76 | 17.0 | 643 | 5 | BU011346 QGJ15P15. |
| 20 | 76 | 17.0 | 669 | 5 | BQ990734 QGF20P11. |
| 21 | 76 | 17.0 | 673 | 5 | BU012409 QGJ1N15.Y |
| 22 | 76 | 17.0 | 692 | 5 | BQ999150 QGG2LE06. |
| 23 | 76 | 17.0 | 692 | 5 | BU014714 QGJ8C12.Y |
| 24 | 76 | 17.0 | 698 | 5 | BQ990122 QGF19I14. |

| | | | | | |
|------|------|------|-----|---|-----------|
| 25 | 76 | 17.0 | 701 | 5 | BQ988151 |
| 26 | 76 | 17.0 | 767 | 5 | BU012833 |
| c 27 | 73.8 | 16.5 | 456 | 5 | CN253987 |
| 28 | 72.8 | 16.3 | 656 | 5 | BU014798 |
| 29 | 71.4 | 16.0 | 582 | 5 | BU012812 |
| 30 | 69.8 | 15.7 | 602 | 5 | BQ981882 |
| 31 | 69 | 15.5 | 356 | 7 | C0553309 |
| 32 | 69 | 15.5 | 374 | 7 | C0553533 |
| 33 | 66.6 | 14.9 | 582 | 5 | BU009853 |
| 34 | 66.6 | 14.9 | 586 | 5 | BU012626 |
| c 35 | 66.4 | 14.9 | 554 | 5 | BU011459 |
| 36 | 66.2 | 14.8 | 411 | 1 | AV786126 |
| 37 | 66.2 | 14.8 | 445 | 1 | AV824429 |
| 38 | 62.6 | 14.0 | 363 | 7 | CN847468 |
| 39 | 62.2 | 13.9 | 516 | 8 | BH581774 |
| 40 | 60.4 | 13.5 | 673 | 8 | BH657225 |
| c 41 | 53 | 11.9 | 918 | 9 | CL504812 |
| 42 | 52 | 11.7 | 371 | 7 | C0749420 |
| c 43 | 51.6 | 11.6 | 721 | 8 | BH4733290 |
| 44 | 49.8 | 11.2 | 379 | 7 | CF270036 |
| 45 | 48.6 | 10.9 | 394 | 4 | BG321454 |

ALIGNMENTS

RESULT 1
BQ989575
LOCUS QGF18A17.YG.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
DEFINITION QGF18A17, mRNA linear EST 21-AUG-2002
ACCESSION BQ989575
VERSION BQ989575.1 GI:22409110
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 604)
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riaseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
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Asmudson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
Belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF18 row: A column: 17.

FEATURES
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Location/Qualifiers
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/cultivar="L.serriola"
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/clones="QG18A17"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCDNASFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG_TISSUE=germinating seeds
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCGTGCGGG

ORIGIN

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Query Match      44.5%; Score 198.6; DB 5; Length 604;
Best Local Similarity 82.0%; Pred. No. 7.5e-43;
Matches 242; Conservative 0; Mismatches 49; Indels 4; Gaps 1;

Qy 155 AGATATCGCATCCCTTGTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 106 AGATATCACGAGTGTGAGAGGAGAACTATGCGAGAAACCTAGCAAGACATGGTCGGGTAA 165

Qy 215 CTGTGGCNAATACGGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
Db 166 CTGTGGCAACACCGGACACTGTGTATGGCCAGTGCANAATCTTTGGAGGGTGGAGCCCATGG 225

Qy 275 AGCGTGTCTATGGGTAAACGGGAAACACATCTGTTTCTGTACTTCAATTGTAATAAAGC 334
Db 226 AGCATGTCACTGGTGGAGGAGAAACACATGTGCTTCTGTACTTAAATTGTCCTAAGC 285

Qy 335 CGAAAGCTTCTCAAGCAAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAAATGC 394
Db 286 TGAAGAAGCTTGCCCAAGACAACTCAAGCCAAAGAGCTGCTCAAGACAACTCAAGC 345

Qy 395 CCRAAGCTTGACCG-----TGATGCCAAGAAGTGGTTCRAAGCTTGAACATCC 445
Db 346 TAAAGAAGCTAGACGGCCATGAGGACAAAGAAGTAGTACCAAAATGTGGACCATCC 400

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RESULT 2

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BQ984300
LOCUS      BQ984300
DEFINITION BQ984300.1 616 bp mRNA linear EST 21-AUG-2002
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           QGE21E24, mRNA sequence.

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ACCESSION

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BQ984300
VERSION    BQ984300.1
KEYWORDS   GI:22401825
SOURCE     Lactuca sativa

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ORGANISM

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Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 616)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

```

REFERENCE

AUTHORS

```

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Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGE21 row: E column: 24.

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FEATURES

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   /mol_type="mRNA"
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   /lab_host="E.coli"

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/clone lib="QG_EFGHJ lettuce serriola"
/notes=Vector: pBRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=germinating seeds
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCGTGCGGG

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ORIGIN

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Query Match      44.2%; Score 197; DB 5; Length 616;
Best Local Similarity 81.7%; Pred. No. 2e-42;
Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;

Qy 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 106 AGATATCACGAGTGTGAGAGGAGAACTATGCGAGAAACCTAGCAAGACATGGTCGGGTAA 165

Qy 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
Db 166 CTGTGGCAACACCGGACACTGTGTATGGCCAGTGCANAATCTTTGGAGGGTGGAGCCCATGG 225

Qy 275 AGCGTGTCTATGGTAAACGGGAAACACATGTTTCTGTACTTCAATTGTAATAAAGC 334
Db 226 AGCATGTCACTGGTGGAGGAGAAACACATGTGCTTCTGTACTTAAATTGTCCTAAGC 285

Qy 335 CGAAAGCTTGTCTCAAGACAAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAAATGC 394
Db 286 TGAAGAAGCTTGCCCAAGACAACTCAAGCCAAAGAGCTGCGCCCAAGACAACTCAAGC 345

Qy 395 CCRAAGCTTGACCG-----TGATGCCAAGAAGTGGTTCRAAGCTTGAACATCC 445
Db 346 TAAAGAAGCTAGACGGCCATGAGGACAAAGAAGTAGTACCAAAATGTGGACCATCC 400

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RESULT 3

BQ984745

LOCUS

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DEFINITION BQ984745.1 620 bp mRNA linear EST 21-AUG-2002
           QGE4H04.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
           QGE4H04, mRNA sequence.

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ACCESSION

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BQ984745
VERSION    BQ984745.1
KEYWORDS   GI:22402270
SOURCE     Lactuca sativa

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ORGANISM

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Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 620)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

```

REFERENCE

AUTHORS

```

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGE4 row: h column: 04.

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TITLE

JOURNAL

COMMENT

Location/Qualifiers

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/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCTGTGCGGG"

ORIGIN
Query Match 44.2%; Score 197; DB 5; Length 620;
Best Local Similarity 81.7%; Pred. No. 2e-42;
Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 106 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 165
QY 215 CTGTGCGCAATACGGGACATTTGACAACTAATGTAATCATCGGAGGTCGGCCCATGG 274
DB 166 CTGTGCGCAATACGGGACATTTGACAACTAATGTAATCATCGGAGGTCGGCCCATGG 225
QY 275 AGCGTGTGCATGTCGTAACGGGAAACACATGTTTCTGTTACTTCAATTTGTAAGGAGC 334
DB 226 AGCATGTGCATGTCGTTGAGGAGAAACACATGTTCTGCTACTTAAATTTGCTTAAGC 285
QY 335 CGAAAGCTTGTCTAAGCAAACTTAAAGCGCAACATCGCTCAAGCAAACTTAATGC 394
DB 286 TGAAGAAGCTTGCCCAAGCAAACTCAAGCGCAAGAGCTCGCCCAAGCAAACTCAAGC 345
QY 395 CCAAAAGCTTGACCG----TGATGCCAAGAAAGTGGTTCCTCAACCTTGAACATCC 445
DB 346 TAAAAGCTAGACCGCCCATGAGGCAAGAAAGTAGTACCAAAATGTGGACCATCC 400

RESULT 4
BU008575 QH7P24.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
LOCUS QH7P24, mRNA sequence.
DEFINITION BU008575.1 GI:22442970
ACCESSION BU008575
VERSION BU008575.1
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 641)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA

FEATURES
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Location/Qualifiers
1. 641
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/cultivar="L. serriola"
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/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_SEQ=Not found"

ORIGIN
Query Match 44.2%; Score 197; DB 5; Length 641;
Best Local Similarity 81.7%; Pred. No. 2e-42;
Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 127 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 186
QY 215 CTGTGCGCAATACGGGACATTTGACAACTAATGTAATCATCGGAGGTCGGCCCATGC 274
DB 187 CTGTGCGCAATACGGGACATTTGACAACTAATGTAATCATCGGAGGTCGGCCCATGC 246
QY 275 AGCGTGTGCATGTCGTAACGGGAAACACATGTTTCTGTTACTTCAATTTGTAAGGAGC 334
DB 247 AGCATGTGCATGTCGTTGAGGAGAAACACATGTTCTGCTACTTAAATTTGCTTAAGC 306
QY 335 CGAAAGCTTGTCTAAGCAAACTTAAAGCGCAACATCGCTCAAGCAAACTTAATGC 394
DB 307 TGAAGAAGCTTGCCCAAGCAAACTCAAGCGCAAGAGCTCGCCCAAGCAAACTCAAGC 366
QY 395 CCAAAAGCTTGACCG----TGATGCCAAGAAAGTGGTTCCTCAACCTTGAACATCC 445
DB 367 TAAAAGCTAGACCGCCCATGAGGCAAGAAAGTAGTACCAAAATGTGGACCATCC 421

RESULT 5
BU0095419 QH7P04.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
LOCUS QH7P04, mRNA sequence.
DEFINITION BU0095419
ACCESSION BU0095419
VERSION BU0095419.1
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 547)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/

```

JOURNAL
COMMENT

Unpublished (2002)
Contact: Alexander Kozik [R.W.Micheltmore]
Department of Vegetable Crops, R.W.Micheltmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [micheltmore@vegmil.ucdavis.edu]
belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF9 row: P column: 04.

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:4236"

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/lab_host="E.coli"

/clone_lib="QG_EFGHJ lettuce serriola"

/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/TAG_TISSUE-germinating seeds
TAG_Lib=QG_EFGHJ lettuce serriola
TAG_SEQ=TCTGTGCGGG"

ORIGIN

Query Match 39.7%; Score 177.2; DB 5; Length 547;

Best Local Similarity 82.6%; Pred. No. 4.6e-37;

Matches 228; Conservative 0; Mismatches 43; Indels 5; Gaps 2;

QY 174 GGAGAACTATCGGAAAGCTAGCAAGACATGGTGGGAAACTGTGGCAATACGGGACAT 233

Db 3 GGAGAACTATCGGAAACCTAGCAAGA-ATGGTCGGTAACTGTGGCAACACGGACAC 61

QY 234 TGTGACACCAATGTAATCATGGAGGTGGGCCCATGGAGGTGTCATGTGCGTAAAC 293

Db 62 TGTGATGCCAGTGCATAATCTTGGAGGTGGGCCCATGGAGCATGTTCACGTGCGTGA 121

QY 294 GGGAAACACATGTGTTCTGTTACTTCAATTTGTAATAAGCGGAAAGCTTGTCTCAAGAC 353

Db 122 GGGAAACACATGTGTTCTGTTACTTCAATTTGTTAAAGCTGAAAGCTTGGCCCAAGAC 181

QY 354 AAATTAAGCGCAACAACTCGCTCAAGACAACTTAATGCCAAAGCTTGCACCG--- 409

Db 182 AAATTAAGCGCAACAACTCGCTCAAGACAACTTAATGCCAAAGCTTGCACCGCGCA 241

QY 410 TGATGCCAAGAAAGTGGTTCACAAAGTTCACATCC 445

Db 242 TGAGCAAGAAGTAGTACCAATGTGGACCATCC 277

RESULT 6

AJ412176

LOCUS

DEFINITION AJ412176 Helianthus annuus cv. Emil protoplast Helianthus annuus cDNA clone HAdp1R101A04, mRNA sequence.

ACCESSION AJ412176

VERSION AJ412176.1

KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

REFERENCE
AUTHORS

Tamborindéguy, C.; Ben, C.; Liboz, T. and Gentsbittel, L.
Sequence evaluation of four specific cDNA libraries for development of sunflower

JOURNAL

Mol. Genet. Genomics 271 (3), 367-375 (2004)

COMMENT

Contact: Gentsbittel L
Laboratoire de Biotechnologie et Amélioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National Supérieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge, Auzeville, CASTANET TOLOSAN 31326, France.

FEATURES

source

1..468

/organism="Helianthus annuus"

/mol_type="mRNA"

/cultivar="Emil"

/db_xref="taxon:4232"

/clone="HAdp1R101A04"

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/clone_lib="Helianthus annuus cv. Emil protoplast"

ORIGIN

Query Match 36.0%; Score 160.6; DB 1; Length 468;

Best Local Similarity 78.1%; Pred. No. 1.4e-32;

Matches 193; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATCGGAAAGCTAGCAAGACATGGTCCGGAAA 214

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QY 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGGAGGTGGGCCCATGG 274

Db 154 ATGTGGCAACACAGACACTGTGATGACCATGTGATGAGGAGGTGAGGCCATGG 213

QY 275 AGCGTGTGATGTCGTTAAACCGGAAACACATGTGTTCTGTACTTCAATTTGTAATAAGC 334

Db 214 AGCTTGTGATGTCGCGGTGGGAAACACATGTGTTCTGTACTTCAACTGTTCCAAAGC 273

QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACACTCGCTCAAGACAACTTAATGC 394

Db 274 CCAGAGTTGCTCAGGATTAATCTCAGACGAGAGAGCTCGCAAGGAGAGATTGAAGC 333

QY 395 CCAAAAG 401

Db 334 CGAAAG 340

RESULT 7

CD846862

LOCUS

DEFINITION DH0AB512E07RM1 HaDevR1 Helianthus annuus cDNA clone HaDevR151E07, mRNA sequence.

ACCESSION CD846862

VERSION CD846862.1

KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

ORGANISM

Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

REFERENCE

1 (bases 1 to 606)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

CONTACT: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme "Genoplatte" (http://www.genoplatte.com

and http://genoplatte-info.infobiogen.fr).

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FEATURES
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        /clone="HadevR151807"
        /tissue_type="leaves"
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ORIGIN
  Query Match      34.6%; Score 154.2; DB 6; Length 606;
  Best Local Similarity 76.5%; Pred. No. 8e-31;
  Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 155 AGATATCGCATCGGTAGTGGAGAACTATGCGAGAAAGCTACAGACATGTCGCGGAAA 214
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QY 97 AGAAATCGGATCGGTGAAAGGAGAAATATGTGAGAGGCAAGCCAGACATGTCGCGGAAC 156
Db 97 |||||
QY 215 CTGTGGCATACGGGACATGTGCACACCAATGTAATCATCGGAGGGTGCAGCCCATGG 274
Db 215 |||||
QY 157 ATGTGGCAAGACAAAACACTGTGTGATGCCAGTGTCTGGAGGGTGCAGCCCATGG 216
Db 157 |||||
QY 275 ACGGTGTATGTGCGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTTGAAAAAGC 334
Db 275 |||||
QY 217 ACCTTGTACAGTGGCGATGGGAAACACATGTGTTCTGTTACTTCAATTTGAAAAAGC 276
Db 217 |||||
QY 335 CGAAAGCTTGTCTAAGCAAACTTAAAGCCGAAACACTCGCTCAAGACAAACTTAAATGC 394
Db 335 |||||
QY 277 CCAGAAAGTTGGCTCAGGATAAATCAGAGCGGAGAGTCTGCCAAGGAGAGATTGAAAC 336
Db 277 |||||
QY 395 CCAAAAG 401
Db 395 |||||
QY 337 CGAAAG 343
Db 337 |||||

RESULT 8
AJ541276
LOCUS AJ541276 HaDpR1 Helianthus annuus cDNA clone HO0003K05, mRNA
DEFINITION
ACCESSION AJ541276
VERSION AJ541276
KEYWORDS AJ541276.1 GI:28370751
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE
1 (bases 1 to 475)
Tamborindéguy, C., Ben, C., Liboz, T. and Gentzbittel, L.
Sequence evaluation of four specific cDNA libraries for
developmental genomics of sunflower
Mol. Genet. Genomics 271 (3), 367-375 (2004)
JOURNAL Contact: Tamborindéguy C
COMMENT Laboratoire de Biotechnologie et Amélioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Supérieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Végétale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOLOSAN 31326, France.

FEATURES
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ORIGIN

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Best Local Similarity 77.5%; Pred. No. 1.1e-30;
Matches 186; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 162 GCATCCGTTAGTGGAACTATGCGAGAAAGCTAGCAAGACATGTCGCGGAAACTGTGCG 221
Db 162 |||||
QY 4 GATCGGTGAAGGAGAAATTTATGTGAGAAAGCAAGACATGTCGCGGAAATGTGCG 63
Db 4 |||||
QY 222 AATACGGGACATTTGTGACAAACCAATGTAAATCATGGAGGGTGCAGCCCATGAGCGTGT 281
Db 222 |||||
QY 64 AACCAAGACACTGTGATGACCCAGTGCAGTCTTGGAGGGTGCAGCCCATGAGCGTGT 123
Db 64 |||||
QY 282 CATGTGCGTAACGGGAAACACATGTGTTCTGTTACTTCAATTTGAAAAAGCCGAAAG 341
Db 282 |||||
QY 124 CATGTGCGCGGTGGGAAACACTTTGTCTTCTGCTACTTCAACTGTTTCAAAAGCCGAGAAG 183
Db 124 |||||
QY 342 CTTGCTCAAGACAAACTTAAAGCCGAAACAACTCGCTCAAGACAAACTTAAATGCCAAAAG 401
Db 342 |||||
QY 184 TTGGCTCAGGATTAATCTCAGACGAGAGAGCTCGCAAGGAGAGAGTTGAAGCCGAAAG 243
Db 184 |||||

RESULT 9
B0844100
LOCUS B0844100
DEFINITION B0844100.1 GI:22224503
ACCESSION B0844100
VERSION B0844100.1
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE
1 (bases 1 to 239)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
COMMENT Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_CA_Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGA12 row: M column: 13.
FEATURES
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        /clone_lib="QG ABCDI lettuce salinas"
        /note="Vector: pBRCDNASFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_SEQ=Not found"

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ORIGIN

| Query Match | 29.4%; | Score 131.2; | DB 5; | Length 239; |
|-----------------------|-----------------|---|-----------|-------------|
| Best Local Similarity | 81.4%; | Pred. No. 1.2e-24; | | |
| Matches 162; | Conservative 0; | Mismatches 36; | Indels 1; | Gaps 1; |
| QY | 155 | AGATATCCGATCCGTTAGTGGAGAACTATCGGAGAAAGCTAGCAAGACATGTCGGGAAA | 214 | |
| Db | 41 | AAATATCAAGAGTGTGAGAGGAGAACTATGTCGAGAAANCTAGNAAAGAAATGTCGGGTAA | 100 | |
| QY | 215 | CTGTGGCAATACGGGACATTTGTGACACCAATCTGTAATCATCGGAGGTTGGCGCCATGG | 274 | |
| Db | 101 | CTGTGNNAAACCCGGACACTGTGATGSCCAGTCAANTCTTGGAGGTTGGAGCCCATGG | 160 | |
| QY | 275 | AGCGTGTCATGTGCGTAAACGGGAAACATCTGTTTCTGTTACTTCAATTGT-AAAAAG | 333 | |
| Db | 161 | AGCATGTCACTGGCGTGGAGGGGAAACACATGTCCTTCTGCTACTTTTAATTGCTCTAAAG | 220 | |
| QY | 334 | CCGAAAAGCTTGTCTCAAGA | 352 | |
| Db | 221 | CTGAAAAGCTTGGCCCAAGA | 219 | |

| | | | | | |
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| RESULT 10 | AJ541406 | 359 bp | mrna | linear | EST 04-MAY-2004 |
| LOCUS | AJ541406 | | | | |
| DEFINITION | AJ541406 | Hadp0r1 | Helianthus annuus | cDNA clone | HO0005105, mRNA |
| ACCESSION | AJ541406 | | | | |
| VERSION | AJ541406.1 | GI:28370881 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Helianthus annuus | | | (common sunflower) | |
| ORGANISM | Helianthus annuus | | | | |

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 359)
Tamborindeguy, C., Ben, C., Liboz, T. and Gentzbittel, L.
Sequence evaluation of four specific cDNA libraries for
developmental genomics of sunflower
Mol. Genet. Genomics 271 (3), 367-375 (2004)
Contact: Tamborindeguy C
Laboratoire de Biotechnologie et Amélioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Supérieure Agronomique de Toulouse
IFR40, Pôle de Biotechnologie Végétale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOULOSAN 31326, France.

| FEATURES | source |
|--|--------|
| <p> <i>mauveville</i>, CASIANET 10LOSAN 31326, France. Location/Qualifiers 1. .359 /organism="Helianthus annuus" /mol_type="mRNA" /cultivar="Emil" /db_xref="taxon:4232" /clone="HQ0005105" /tissue_type="hypocotyl" /cell_type="protoplast" /dev_stage="1- to 5-days old protoplast" /clone_lib="Hapshot" </p> | |

ORIGIN

| | Query Match | 28.5% | Score 127; | DB 1; | Length 359; |
|----|-----------------------|---|--------------------|-----------|-------------|
| | Best Local Similarity | 77.4% | Pred. No. 1.7e-23; | | |
| | Matches 154; | Conservative 0; | Mismatches 45; | Indels 0; | Gaps 0; |
| QY | 205 | GGTCGGGAAACTGTGGCAATACGGGCAATTGTGACCAACCAATGTAAATCATGGGAGGGTG | 264 | | |
| Db | 4 | GGTCGGGAAATGTGGCAACACACAAGACACTGTGACGACCAGTGCAGTCTTTGGGAGGGTG | 63 | | |
| QY | 265 | CGGCCCATGGAGCGGTGTCATGTGCGTAACGGGAAACACATGTGTTCTGTACTTCAATT | 324 | | |
| Db | 64 | CAGCCCATGGAGCTTGTCACTGGCGGGTGGGAAACACATGTGCTTCTGTACTTCAACT | 123 | | |


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ACCESSION   BQ847005
VERSION     BQ847005.1  GI:22230770
KEYWORDS    EST.
SOURCE      Lactuca sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1 (bases 1 to 603)
AUTHORS    Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
            Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
            Ellison, P., Koltman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
            Lai, Z., Church, S., Jackson, B. and Bradford, K.
            Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
            Unpublished (2002)
            Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmudson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozikeatgc.org [michelmore@vegmil.ucdavis.edu]
            belongs to contig QG_CA_Contig6866, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGA20 row: O column: 20.
FEATURES    Location/Qualifiers
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                from 10 different sources of RNA from a single genotype.
                Separate cDNAs were generated using primers that
                incorporated unique 5' and 3' tags to distinguish each
                source of RNA. cDNAs were then pooled, size-fractionated,
                directionally cloned into a custom medium-copy vector and
                transformations made with four size classes to minimize
                size bias. Details of each source of RNA and library
                construction can be obtained at http://cgpdb.ucdavis.edu/
                TAG TISSUE=germinating seeds
                TAG_LIB=QG ABCDI lettuce salinas
                TAG_SEQ=TCCTGTGCGGG"
ORIGIN
Query Match      27.7%; Score 123.6; DB 5; Length 603;
Best Local Similarity 71.8%; Pred. No. 1.6e-22;
Matches 204; Conservative 0; Mismatches 74; Indels 6; Gaps 3;
QY 168 GTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGAAACTGTGGCAATAGC 227
DB 121 GTGATAGGAGAACTATGTGAGAAAGCTACTTGGGACTGGACCGCTAACATGTGTGAACACC 180
QY 228 GGACATTTGTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGGAGCGTGTATGTG 287
DB 181 GGACACTGAGTGGTTCAGTGCAGAACTTGTGAGGGTGTAGCCCTGGAGCATGTGCTTGTG 240
QY 288 CGTAACGGGAA-ACACATGTGTTTCTG-TTACTTCAATTGTAAAAAGCCGAAAAGCTTGTG 345
DB 241 CGTGGAGGGAAGACACGTCGAGCTTCTCGCTACTTTTATTGTCTTAAAGCTGAAGAGCTTG 300
QY 346 CTCAGACAAACTTAAAGCCGAAACAACTGCTCTCAAGACAAACTTAATGCCCAAAAGCTTGTG 405
DB 301 CCCTTTGACTGACTCAGAGCCAAAGAGCTCGCCCAAGACAAACTCAAGCTCAAAAAGCTAG 360
QY 406 ACCG---TGATGCCAAGAAAGTGGTTCCAAACGTTGACATCC 445
DB 361 ACCGGCCATGAGACAAAGAAAGTAGTACCAGAAATGTGGACCATCC 404

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RESULT 13
LOCUS    AU306450
DEFINITION AU306450 zinnia cultured mesophyll cell equalized cDNA Zinnia
            elegans cDNA clone Z16034, mRNA sequence.
ACCESSION AU306450
VERSION   AU306450.1  GI:41122386
KEYWORDS  EST.
SOURCE    Zinnia elegans
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Zinnia.
            1 (bases 1 to 447)
AUTHORS    Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,
            Matsuoka, N., Minami, A., Nagata-Hiwatashi, M., Nakamura, K.,
            Okamura, Y., Sasea, N., Suzuki, S., Yazaki, J., Kikuchi, S. and
            Fukuda, H.
            Visualization by comprehensive microarray analysis of gene
            expression programs during transdifferentiation of mesophyll cells
            into xylem cells
            Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
            Contact: Taku Demura
            Morphogenesis Research Group
            RIKEN Plant Science Center
            1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9605
            Fax: 81-45-503-9573
            Email: demura@postman.riken.go.jp
            This clone was obtained at our laboratory
            Seq primer: M13 forward.
FEATURES    Location/Qualifiers
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                /clone_lib="zinnia cultured mesophyll cell equalized cDNA"
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Matches 160; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 196 GCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCAT 255
DB 1 GTAAGACATGTCGGGAAATTTGTGCAACACAGACACTGCGATGACGATGCAAGTCCT 60
QY 256 GGGAGGGTGGCGCCCATCGAGCGTGTCTCATGCGTAAACGGGAAACACATGTTTCTGTT 315
DB 61 GGGAGGGTGCAGCTCATGTTGTTGTCACGTGCGCGTGGGAAACACATGTTCTGCT 120
QY 316 ACTTCAATTGTAAAAAGCCGAAAAGCTT-GCTCAAGACAAACTTAAAGCCGAAACATC 374
DB 121 ACTTCAATTGTCAAAGCCGAGAGGTTGGCTCAGGATAAACTCAAAGCAGAAGAGCTC 180
QY 375 GCTCAAGACAAACTTAAATGCCCAAAA 400
DB 181 GCNAGGAGAGAGATTGATGCTGGAAA 206

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RESULT 14
LOCUS    AJ412470
DEFINITION AJ412470 Helianthus annuus cv. Email protoplast Helianthus annuus
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ACCESSION AJ412470
VERSION AJ412470.1 GI:15005725
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; campanulids; Asterales; Asteraceae; Asteroideae;
          Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 487)
AUTHORS Tamborindéguy C., Ben C., Liboz T. and Gentzbittel L.
TITLE Sequence evaluation of four specific cDNA libraries for
JOURNAL development of genomics of sunflower
COMMENT Mol. Genet. Genomics 271 (3), 367-375 (2004)
Contact: Gentzbittel L
Laboratoire de Biotechnologie et Amélioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Supérieure Agronomique de Toulouse
IFR40, Pôle de Biotechnologie Végétale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOLOSAN 31326, France.
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Matches 162; Conservative 0; Mismatches 83; Indels 2; Gaps 1;
QY 155 AGATATCCATCCGTTAGTGGAGACTATGCGAGAACTGCGAGAACTAGCAAGACATGTCGGGAAA 214
Db 110 AGAAATCGGTACGGGGAAGGAGATTAATGTGAGAGGCAAGCAAGCAAGCGGAAA 169
QY 215 CTGTGGCAATACGGGACATTTGTACACCAATGTAATCATGGAGGTCGGCCCATGG 274
Db 170 AGGGGCAACACAGACATTTGTGGACCGGCAAGTTTAGGAGGTCGAGCCCTGG 229
QY 275 AGCGTGTATGTGCGTAAACGGAAACACATGTGTTTCTGTTACTTCAATTTGAAAAAGC 334
Db 230 AGTTGTTTCATGTGCGCGGGGAAACACTTTGTTTGTAGTAAATACAAATATTACCAAGC 289
QY 335 CGAAAGCTTGTCAAGACAACTTAAGCCGAACTCCCTCAAGACAACTTAATGC 394
Db 290 CCAGAG--TAGGTGAGTAAATACAGAGCAGAGAGTACGCCAAGGAGAAATTAGAAGC 347
QY 395 CCAAAAG 401
Db 348 CGAAAAA 354
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DEFINITION QGAL6N20.yg.ab1 QG ABCDI lettuce salinas Lactuca sativa cDNA clone
ACCESSION BQ845488
VERSION BQ845488.1 GI:22227399
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
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          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
          Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 340)
AUTHORS Kozik A., Michelmore, R.W., Knapp S., Matvienko, M., Rieseberg, L.,
          Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
          Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
          Lai, Z., Church, S., Jackson, L. and Bradford, K.
          Lettuce and Sunflower ESTs from the Compositae Genome Project
          http://compgenomics.ucdavis.edu/
          Unpublished (2002)
          Contact: Alexander Kozik [R.W.Michelmore]
          Department of Vegetable Crops, R.W.Michelmore Lab
          University of California at Davis (UCD)
          Amundson Hall, UCD, Davis, CA 95616, USA
          Tel: 1-(530)-742-1742
          Fax: 1-(530)-752-9659
          Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
          belongs to contig QG_CA_Contig238, see http://cgpdb.ucdavis.edu/
          for details.
          Plate: QGAL6 row: N column: 20.
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            from 10 different sources of RNA from a single genotype.
            Separate cDNAs were generated using primers that
            incorporated unique 5' and 3' tags to distinguish each
            source of RNA. cDNAs were then pooled, size-fractionated,
            directionally cloned into a custom medium-copy vector and
            transformations made with four size classes to minimize
            size bias. Details of each source of RNA and library
            construction can be obtained at http://cgpdb.ucdavis.edu/
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            TAG_SEQ=TGTAGCCGGG"
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          Matches 124; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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          Db 1 AGGGTGCAGCCCATGGAGCTTGCCACGTGCGTGGAGGAAACACATGTGCTTCTGCTACT 60
          QY 319 TCAATTGTAATAAAGCCGAAAAGCTTGCTCAAGACAACTTAAAGCCGAACTCGCTC 378
          Db 61 TCAACTGTTTCAAAAAGCAGAGAGATGGCTCAAGATAAGCTGAAAGCCAAAGAGCTCACCA 120
          QY 379 AAGACAAACTTAATGCCAAAAGCTTGACCGTGATGCCAAGAAGTGGTTCCTCAA 432
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